

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2005, 17:54:03 ; Search time 6197 Seconds
(without alignments)
3588.986 Million cell updates/sec

Title: US-09-967-237A-2

Perfect score: 2424

Sequence: 1 MAPICPSPWMLPLIPAPAPG.....RRGTGGSVSRPAEVAENGA 459

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=GenEmbl -QMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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Database :

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3: gb_in.*
4: gb_om.*
5: gb_ov.*
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7: gb_pn.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ets.*
12: gb_ey.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	2424	100.0	1519	9	HAJ10588 Homo sapi
2	2424	100.0	1522	6	AR074439 Sequence
3	2424	100.0	1522	6	AR081119 Sequence
4	2424	100.0	1522	6	AR085316 Sequence

5	2424	100.0	1522	6	AR088064 Sequence
6	2424	100.0	1522	6	AR104223 Sequence
7	2424	100.0	1522	6	AR143487 Sequence
8	2424	100.0	1522	6	AR171392 Sequence
9	2424	100.0	1522	6	AR171563 Sequence
10	2424	100.0	1522	6	BD243152 MN gene a
11	2424	100.0	1552	6	COB84035 Sequence
12	2424	100.0	1552	6	AX330007 Sequence
13	2424	100.0	1552	6	AX332607 Sequence
14	2424	100.0	1552	6	AX333244 Sequence
15	2424	100.0	1552	6	AX336174 Sequence
16	2424	100.0	1552	6	HSMATUMN
17	2424	100.0	1639	9	BC014950 Homo sapi
18	2239	92.4	1289	6	CO726696 Sequence
19	2227	91.9	1399	6	AR095263 Sequence
20	1596	65.8	1965	10	MW0245857
21	1449	51.5	187856	9	AF334829
22	1187	49.0	88328	9	AL357874
23	1176.5	48.5	10898	6	AR074442
24	1176.5	48.5	10898	6	AR081122
25	1176.5	48.5	10898	6	AR085319
26	1176.5	48.5	10898	6	AR088067
27	1176.5	48.5	10898	6	AR104226
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30	1176.5	48.5	10898	6	AR171566
31	1176.5	48.5	10898	6	BD243155
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35	737.5	30.4	6521	6	CO806582
36	737.5	30.4	6521	6	AX795690
37	737.5	30.4	6521	6	AX822141
38	737.5	30.4	6521	6	AX825781
39	714	29.5	415	6	AR074454
40	714	29.5	415	6	AR081134
41	714	29.5	415	6	AR085331
42	714	29.5	415	6	AR088079
43	714	29.5	415	6	AR104238
44	714	29.5	415	6	AR143502
45	714	29.5	445	6	AR171406

ALIGNMENTS

RESULT 1	HAJ10588	1519 bp	mRNA	PRI 23-MAR-2000
LOCUS	Homo sapiens mRNA for renal cell carcinoma associated antigen G250.			
DEFINITION	AJ010588			
ACCESSION	AJ010588.1	GI:7327887		
VERSION	renal cell carcinoma associated antigen G250.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1			
AUTHORS	Grabmaier, K., Vlasers, J.L., de Weijert, M.C., Oosterwijk, M.A., van Bokhoven, A., Brakenhoff, R.H., Noessner, E., Mulders, P.A., Merks, G., Fijdor, C.G., Adema, G.J., and Oosterwijk, E.			
TITLE	Molecular cloning and immunogenicity of renal cell carcinoma-associated antigen G250			
JOURNAL	Int. J. Cancer 85 (6), 865-870 (2000)			
MEDLINE	20175464			
PubMed	10709109			
REFERENCE	2 (bases 1 to 1519)			
AUTHORS	Oosterwijk, E.			
TITLE	Direct Submission			
JOURNAL	Submitted (26-AUG-1998) Oosterwijk E., St. Radboud Academic Hospital Nijmegen, Urological Research Laboratory, Postbus 9101, 6500 HB Nijmegen, THE NETHERLANDS			
FEATURES	location/Qualifiers			
source	1..1519			

ORGANISM Unknown.
Unclasseified.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL Patent: US 5955075-A 1 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..1522
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	6.65e-118	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-967-237a-2 (1-459) x AR074439 (1-1522)

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QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGCAACGTCTCTGTCACTGTCTGTGATGCCGTGCATCCCAAGGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATGCAAGAGATTCCTCCCTTGAGAGAGCTCTTCGGGGAAGATGACCACTG 192
QY 61 GlyGlnGluAspLeuProSerGlyGluAspSerProArgGlnGluAspProProGlyGlu 80
Db 193 GGCAGAGAGATCTGCCAGATGAAGATTCACCCAGAGAGAGATCCACCCGAGAG 252
QY 81 GlnuAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGluValLysPro 100
Db 253 GAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAGTTAAGCT 312
QY 101 LysSerGlnGlnGlnGlySerLeuLysLeuGluAspLeuProThsValGlnuAlaProGly 120
Db 313 AAATCAGAAAGAGAGGCTCCCTGGAATTAGAGATCTACCTACTGTTGAGGCTCTCGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspGlyGlnGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCAAGATTAATGCCACAGGACAAAGAGGATGACACAGATCAT 432
QY 141 TTPATGTYTGTGlyAspProProTTrpProArgValLysProAlaCysAlaGlyArgPhe 160
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QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
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QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnArgHis 200
Db 553 GAATCCTCGGGCTTCCAGACTCCGCGCTCCAGAACTGCGGCTCGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLysLeuGlnuMetAlaLeuGlyProGlyArgGlnLyr 220
Db 613 AGTGTGCAACTGACCTCTCTCGGCTAGAGATGCTGTGGGTCCCGGGCGGAGATAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisArgProGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CGGGCTCTGCAAGCTCATCTGCACTGGGGGCTGAGAGTCTGCGGGCTCGAGACACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnuLysValLysValHisLeuSerThrAlaPheAla 260
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QY 261 ArgValaAspGlnuAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
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QY 281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnuLysAla 300
Db 853 GAGGGCCCGGAAGAAACAGTGCCATATGAGCATGTGTCTGCTCGCTTGGAGAAATCGCT 912
QY 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerArg 320
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QY 321 PheSerArgTyrPheGlnTyrGlnuLysSerLeuThrTrpProProCysAlaGlnuLysVal 340
Db 973 TTCACCCCTACTTCCATATAGAGGATCTCTGACTACACCGCCCTGTGGCCAGGATGC 1032
QY 341 ILeTTPThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisArgLeuSer 360
Db 1033 ATCTGCACTGTGTTTAAACAGACAGTGAATGCTGATGCTTAAGCAGCTCCACCTCTCT 1092
QY 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
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QY 381 LeuAsnGlyArgValLysGlnuLysPheProAlaGlyValaAspSerProArgAla 400
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Db 1213 GCTGAGCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGATCATCTGACCTGTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTGTGCTGCACAGGCTCGCGTCTCTTGCAAGATGAAGACAGACAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGlnuValaAlaGlnuThrGlyAla 459
Db 1333 AGGGAGACCAAGGGGATGTAGCTTACCGCCAGCAGAGTATGCCAGACTGGAGCC 1389

RESULT 3
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LOCUS AR081119
DEFINITION Sequence 1 from patent US 5972353.
ACCESSION AR081119
VERSION AR081119.1 GI:10007847
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclasseified.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL Patent: US 5972353-A 1 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..1522
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ORIGIN

Alignment Scores:

Pred. No.:	6.65e-118	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-967-237a-2 (1-459) x AR081119 (1-1522)

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Qy      41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db      133 CCCCAGATGACAGAGGATTCCTCCCTGGAGAGGCTCTTCGGGGGAAGATGACCCACTG 192
Qy      61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db      193 GGGAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGGAGAG 252
Qy      81 GluAspLeuProGlyGlnGluAspLeuProGlyGlyGluAspLeuProGlyValPro 100
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Qy      101 LysSerGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
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Db      373 GATCTCAAGAAACCCCAAAATATGCCCACAGGACAAAGAGAGATGACAGAGTCAT 432
Qy      141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db      433 TGGGGCTATGAGAGCGACCGGCCCTGGCCCCGGGTGTCCCAAGCTGCGGGGCGCTTC 492
Qy      161 GlnSerProValAspLysLeaArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
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Qy      181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlyHis 200
Db      553 GAACCTCTGGGGCTTCCAGCTCCGCCCTCCAGAACTGGCGCTCGCCCAAAATGGCCAC 612
Qy      201 SerValGlnLeuThrLeuProProGlyLysGlnMetAlaLeuGlyProGlyArgGlyTyr 220
Db      613 AGTGTCAACTGACCTGCTCCCTGGGCTAGAGATGCTCTGGGTTCGCCGGGCGGAGTAC 672
Qy      221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyValAlaAlaGlyArgProGlySerGlnHisThr 240
Db      673 CGGGCTCTGACAGCTGCACTGCACTGGGGGCTGCAAGTGTCTCGGGCTCGAGCACACT 732
Qy      241 ValGlnGlyHisArgPheProAlaGlnLeuHisValValHisLeuSerThrAlaPheAla 260
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Qy      261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLysAlaValLeuAlaAlaPheLeuGln 280
Db      793 AGAGTTACAGAGGCTTGGGGGCGCCGGAGGCGCTGGCCCGGTGGCGCTTCTTGAGAG 852
Qy      281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnLeuAla 300
Db      853 GAGGGCCCGGAAAGAAACAGTGTCTATGAGCAGATGTGCTGTCTGCTTGGAAAGAAATGCT 912
Qy      301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
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Db      973 TTCAGCGCGTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGC 1032
Qy      341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
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Qy      361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
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Db      1273 GGCTCTCTTTTCTGTCTGACACGCTGCGCTTCTTGTGAGATGAGAGGACGACAGA 1332
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LOCUS
DEFINITION
ACCESSION
AR085316
VERSION
AR085316.1 GI:10012085
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1522)
Zavada,J., Pastorekova,S. and Pastorek,J.
AUTHORS
TITLE
MW-specific antibodies and hybridomas
Patent: US 5981711-A 1 09-NOV-1999;
JOURNAL
FEATURES
Location/Qualifiers
1..1522
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ORIGIN

Alignment Scores:
Pred. No.: 6,65e-118 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
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US-09-967-237A-2 (1-459) x AR085316 (1-1522)

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Db      73 CTCACGTGTGCAACGCTGCTGTCTACTGCTTGTGATGCTGTGCATCCCGAGAGTTG 132
Qy      41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db      133 CCCCAGATGACAGAGGATTCCTCCCTGGAGAGGCTCTTCGGGGGAAGATGACCCACTG 192
Qy      61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db      193 GGGAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGGAGAG 252
Qy      81 GluAspLeuProGlyGlnGluAspLeuProGlyGlyGluAspLeuProGlyValPro 100
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Qy      101 LysSerGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db      313 AAATCAGAAAGAGGGGCTCCCTGAAGTTAGAGATCTACTGTTGAGGCTCTCGA 372
Qy      121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
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Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCYsProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGCTGGATATCCGCCCAAGCTCCGCCCTTCTGCGGCCCTGCGGCCCTTG 552
Qy 181 GluLeuLeuGlyPheGlnLeuPheProLeuPheProGluLeuArgLeuArgAsnAsnGlyHis 200
Db 553 GAACCTCGGGGCTTCACAGCTCCCGCGCTCCCAAGAACGCGCTCGCAAGCAATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyYArGluYr 220
Db 613 AGTGTCAACTGACCCCTCTCTGGGCTAGAGAGTGTCTGGGGTCCGGGGGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleTropGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 673 CGGGCTCTGACGCTGCACTTGCACTGGGGGGCTGCAAGTGTCTCGGGCTCGAGCAACT 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValHisIleLeuSerThrAlaPheAla 260
Db 733 GTGGAGGSCAACCGTTTCCCTGCGAGATCCAGTTCACCTCAGCACCGCCCTTGGC 792
Qy 261 ArgValAspGluAlaLeuGlyYArGProGlyYLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGGGGCCGGGAGGCTCGGGTGTGGCCCTTCTTGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAla 300
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Qy 361 AspThrLeuTyrGlyProGlyYAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
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Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGGCTCTTTTGTGCTGCTCACACGCTCGGCTTCTGTGGAGATAGAAAGGAGCAGCA 1332
Qy 441 ArgGlyThrIYrGlyGlyValSerTyrArgProAlaGluValAlaGlnThrGlyAla 459
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RESULT 5
AR088064 1522 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5989838.
ACCESSION AR088064
VERSION AR088064.1 GI:10014827
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 1 23-NOV-1999;
FEATURES
source location/Qualifiers
1..1522
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ORIGIN
Alignment Scores:
Pred. No.: 6.65e-118 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-967-237A-2 (1-459) x AR088064 (1-1522)

Qy 1 MetaLapProLeuCYsProSerProTProLeuProLeuLeuIleProAlaProAlaProGly 20
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Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetCProValHisProGlnArgLeu 40
Db 73 CTCACTGTCAACTGCTGCTGTCACTGCTGTCTGATGCTTCATCCCAAGAGTTTG 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCGGAGTGCAGAGAGATCCCTTGGAGAGGCTTCTGGGAGAGATGACCCACTG 192
Qy 61 GlyGluGluAspLeuProSerGluGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 193 GCGCAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCGGAGAG 252
Qy 81 GluAspLeuProGlyGlyGluAspLeuProGlyGluGluAspLeuProGlyValIYsPro 100
Db 253 GAGGATCTACTCGAGAGAGAGATCTACTGAGAGAGAGATCTACTGAAGTTAAGCT 312
Qy 101 LysSerGluGluGlySerLeuLeuLeuAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGGGCTCTCTGAAGTTAAGATCTACTGTTGAGGCTCTGGA 372
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspIYsGluGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCAAGATTAATGCCACAGGACAAAGAGGAGTGAACAAGTCTAT 432
Qy 141 TTPATGYTGYGlyYAspProProTProArGVaLserProAlaCYaLAgLYArGhe 160
Db 433 TGGCGCTATGAGAGCACCCTCGGCTGGGGTGTCTCCAGAGCTGCGGGCGGCTTC 492
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCYsProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGCTGGATATCCGCCCAAGCTCCGCCCTTCTGCGGCCCTGCGGCCCTTG 552
Qy 181 GluLeuLeuGlyPheGlnLeuPheProLeuPheProGluLeuArgLeuArgAsnAsnGlyHis 200
Db 553 GAACCTCGGGGCTTCACAGCTCCCGCGCTCCCAAGAACGCGCTCGCAAGCAATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyYArGluYr 220
Db 613 AGTGTCAACTGACCCCTCTCTGGGCTAGAGAGTGTCTGGGGTCCGGGGGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleTropGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 673 CGGGCTCTGACGCTGCACTTGCACTGGGGGGCTGCAAGTGTCTCGGGCTCGAGCAACT 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValHisIleLeuSerThrAlaPheAla 260

Db 733 GTGAAAGCCACCGCTTCCCTGCCAGATCCAGTGGTTCACCTCAGACCGCCTTTGCC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTACAGAGGCTTTGGGGCGCCCGGAGGCTTGCGCTTTGGCGCCTTTCTGGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGluLeuSerArgLeuGluGluAla 300
Db 853 GAGGGCCCGGAAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGGAAAGAAATCGCT 912
Qy 301 GluGluGlySerGluThrGluValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGTCCAGAGCTGACATATCTGCACTTCCTGCTGAC 972
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCAAGCCGCTACTTCCAAATATGAGGGGTCTTGACTACACCGCCCTTGCCAGGGTGC 1032
Qy 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGluLeuHisThrLeuSer 360
Db 1033 ATCTGACTGTGTTTAAACAGACAGTATGCTGATGCTGAAGCAGCTCCACACCTCTCT 1092
Qy 361 AspThrLeuTyrProGlyAspSerArgLeuGluLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGACCTGGTGACTCTCGCTACAGCTGAACCTTCCAGCGAGCGACGCT 1152
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGAGAGATTGAGGCTCTTCCCTGCTGAGTGCACACAGATCCCTGGGCT 1212
Qy 401 AlaGluProValGluLeuAsnSerCysLeuAlaAlaGlyAspLysLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGACATCTTACGCCCTGGTTT 1272
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTCTTTTGTGTGCACAGCGTGCCTTCTTGTGAGATGAAGAAGCGCACAGAGA 1332
Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAAACCAAGCGGTGTGAGCTACGCCCAAGCAAGTACCGAGACGTGAGGCC 1389
RESULT 6
AR104223 1522 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 1 from patent US 6093548.
DEFINITION AR104223
ACCESSION AR104223
VERSION AR104223.1 GI:12816931
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 1 25-JUL-2000;
FEATURES
source 1..1522
location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 6.65e-118 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-967-237a-2 (1-459) x AR104223 (1-1522)
Qy 1 MetAlaProLeuCySPSerProTrrPLeuProLeuLeuIleProAlaProAlaProGly 20

Db 13 ATGAGTCTCCCTGTGCCCCCAGCCCCCTGGCTCTCTGTGTGATCCCGGGCCCTGTCCAGGC 72
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGGAACTGCTGCTGTGATCTGCTCTTGTATGCTGTCTCATCCCGAGAGGTTG 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCGGATGCAGAGGATTCCTCCCTTGGAGGAGGCTCTTCTGGGAAATGACCCACTG 192
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 193 GCGAGAGGATGTGCCCACTGAAGAGATTCACCAAGAGAGAGATTCACCCGGAGAG 252
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGlyGluAspLeuProGlyValLysPro 100
Db 253 GAGGATTCACCTGAGAGAGAGGATCTACCTGGAGAGAGAGATCTACTGAAGTTAACTC 312
Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGAGGCTCCTGAAGTTAGAGGATCTACTACTGTGAGGCTCTCGGA 372
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 373 GATCTCTAAGAACCCCAAGATTAATGCCACAGAGGACAAAGAGGAGATGCACAGATCAT 432
Qy 141 TrpArgTyrGlyGlyAspProProTrrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGAGAGCGACCGCCCTGCGCGGGGTGTCCCAAGCTGCGGGGCGCGCTTC 492
Qy 161 GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTGTGCCCGGCGCCGCCCTG 552
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnArgHis 200
Db 553 GAACTCTGGGCTTCCAGCTCCGCGCGCTCCAGAACTGGCGCTGGCAACAATGGGCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 613 AGTGTGAACTGACCTCGCTCTCGGGCTAGAAATGGCTTGTGGTCCCGGGCGGAGTAC 672
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrrPylAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CGGGCTCTGACGTGATCTGCATCTGGGGGGCTGCAGTGTGTCCGGGCTTGGAGCACAT 732
Qy 241 ValGluGlyHisArgPheProAlaGluLysValAlaHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTCCTGCTCGAGATCCAGTGGTTCACCTCAGACACGCGCTTGGC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTACAGAGGCTTTGGGGCGCCCGGAGGCTTGCGCTTTGGCGCCTTTCTGGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGluLeuSerArgLeuGluGluAla 300
Db 853 GAGGGCCCGGAAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGGAAAGAAATCGCT 912
Qy 301 GluGluGlySerGluThrGluValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGTCCAGAGCTGACATATCTGCACTTCCTGCTGAC 972
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCAAGCCGCTACTTCCAAATATGAGGGGTCTTGACTACACCGCCCTTGCCAGGGTGC 1032
Qy 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGluLeuHisThrLeuSer 360
Db 1033 ATCTGACTGTGTTTAAACAGACAGTATGCTGATGCTGAAGCAGCTCCACACCTCTCT 1092
Qy 361 AspThrLeuTyrProGlyAspSerArgLeuGluLeuAsnPheArgAlaThrGlnPro 380

Db	1093	GACACCTCTGTGGGACCTGGTACTCTCGGCTACAGCTGAACCTTCCAGCAGCAGCCT	1152
Qy	361	LeuAngiYArgValIIEgluAlaSerPheProAlaGlyValAspSerSerProArgAla	400
Db	1153	TTGAATGGGCGAGTATTGAGGCCCTCTTCCCTGCTGGAAGTGAACAGCAGTCTTGCGCT	1212
Qy	401	AlaGluProValGlnLeuAsnSerCysIleuAlaAlaGlyAspIleuAlaLeuValPhe	420
Db	1213	GCTGAGCCAGCTCCAGCTCAATTCCCTGCGCTGCTGCTGATCATCTTACGCCCTGGTATT	1272
Qy	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1273	GAGCTCTTTTGTGCTGTACCAAGCCTCGCTTCTTGTCAGATAGAAGCAGCAGACA	1332
Qy	441	ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGlyThrGlyAla	459
Db	1333	AGGGGAACCAAGGGGGGTGTAGCTACCGCCACAGACAGATGACCGGAGACTGGAGCC	1389
RESULT 7			
LOCUS	ARI43487	1522 bp	DNA
DEFINITION	Sequence 1 from patent US 6204370.		linear
ACCESSION	ARI43487		
VERSION	ARI43487.1		GI:15104773
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1522)		
TITLE	Zavada,J., Pastorekova,S. and Pastorek,J.		
JOURNAL	MN gene and protein		
FEATURES	Patent: US 6204370-A 1 20-MAR-2001;		
source	Location/Qualifiers		
	1..1522		
	/organism="unknown"		
ORIGIN	/mol_type="unassigned DNA"		
Alignment Scores:			
Pred. No.:	6,65e-118	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
Db:	6	Gaps:	0
US-09-967-237A-2 (1-459) x ARI43487 (1-1522)			
Qy	1	MetAlaProLeuCysProSerProTyrLeuProLeuLeuIleProAlaProAlaProGly	20
Db	13	ATGGGTCCCTGTGGCCCAAGCCCTGGCTCCTCTGTGATCCCGGCCCTGCTCAAGC	72
Qy	21	LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu	40
Db	73	CTCACTGTGCAACTGCTGCTGTCACTGCTTGTGAAGCCGTGTCATCCCAAGAGTTG	132
Qy	41	ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu	60
Db	133	CCCCGAGTGCAGAGATTCCCCCTTGGAGAGGCTTTCTGGGGGAAGATGACCCACTG	192
Qy	61	GlyGluGluAspLeuProSerGlnGluAspSerProArgGluAspProProGlyGlu	80
Db	193	GGCAGAGAGATCTGCCAAGTGAAGAGATTCAACCAAGAGAGAGATCCACCCGAGAG	252
Qy	81	GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGluValIysPro	100
Db	253	GAGGATCTAAGTGCAGAGAGAGATCTAAGTGAAGAGAGAGATCTAAGATTAAAGCT	312
Qy	101	LysSerGlnGlnGlnGlySerLeuYrLeuGluAspLeuProThrValGluAlaProGly	120
Db	313	AAATCAGAAAGAGGGCTCCCTGAAGTTAAGAGATCTAAGCTGTTGAAGGCTTCGGGA	372
Qy	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis	140

Db	373	GATCCTCAAGAACCCCAAGATAATGCTCCACAGGGCAAAAGGGGATGACCAAGATCAT	432
Qy	141	TRPAQTYRGLYGLYAAPPProTTPProArqValSerProAlaCyAlaGlyARpPhe	160
Db	433	TGGCGCTATGAGAGCGAACCCCGCCTGGCCCGGGGTGTCCCAAGCTGGCGGGCGCGCTTC	492
Qy	161	GLnSerProValAspIleArgProGlnLeuAlaAlaPheCySProAlaLeuArgProLeu	180
Db	493	CAGTCCCGGGTGGATATATCCGCCCCACAGCTCCCGCTTCTCCCGGGCCCTCGCCCTCG	552
Qy	181	GLileuLeuGlyPheGlnLeuProProLeuProGlnLeuAlaArgAlaAsnArgLys	200
Db	553	GAACCTCCGGGGCTTCCAGCTCCCGCGCTCCCAAACTGCAGCCCTGGCGAAACAAATGGCCAC	612
Qy	201	SerValGlnLeuThrLeuProProGlnYleuGlnMetAlaLeuGlyProGlnYARGLuTYR	220
Db	613	AGTGTGCACACTGACCCCTTCCTCTCGGGCTAAAGATGGCTCTGGGTCCCGGGCGGGAGTAC	672
Qy	221	ArgAlaLeuGlnLeuHisAlaLeuHisSTPGLYAlaAlaArgYARProGlySerGlnHisThr	240
Db	673	CGGGCTTGACAGCTGCATCTGACACTGGGGGGCTGCAGAGTCTGCGGGCTCGAGACACACT	732
Qy	241	ValGluGlyHisArgPheProAlaGluIleHisValValHisIleuSerThrAlaPheAla	260
Db	733	GTGGAAAGCCACCGCTTCTCCCTGCGAGATCCACAGTGGTTCACCTTCAGACACGCGCTTGGCC	792
Qy	261	ArgValaAspGluAlaLeuGlyYARProGlyGlyLeuAlaValaAlaPheLeuGlu	280
Db	793	AGAGTTGACGAGGCTTGGGGCGCCCGGAGAGCTGGCCGCTGTGGCCGCTTCTGGAG	852
Qy	281	GLuGlyProGluGluAsnSerAlaTYRGLuGlnLeuLeuSerArgLeuGluIleAla	300
Db	853	GAGGGCCCGGAGAAACACAGTGCCTATGACAGTTGCTGCTCGCTTGGAGAAATGCT	912
Qy	301	GLuGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	913	GAGGAGAGCTCAGAGACTCAGGTCCCGAGACATGACATATCGACACTCTCCCTCGAC	972
Qy	321	PheSerArgYRrPheGlnTYRGLuGlySerLeuThrThrProProCyAlaGluGlyVal	340
Db	973	TTGAGCCGCTACTTCCAAATGATGAGGGGTCTGTGACTACACCGCCCTGTGGCCAGGGTGTG	1032
Qy	341	IleTPRThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisSThrLeuSer	360
Db	1033	ATCTGGACTGTGTTTAACACACAGTATGTGTAGTGTCAAGCACTCCACACCTCTCT	1092
Qy	361	AspThrLeuTPRGLYProGlyYAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
Db	1093	GACACCTCGTGGGGACCTGTGACTCTCGGCTACAGCTGACACTTCCGAGCAGCAGCACT	1152
Qy	381	LeuAsnGlyAArgValIleGluAlaSerPheProAlaGlyValaAspSerSerProArgAla	400
Db	1153	TTGATATGGCCAGAGATTTGAGGCTCTCTCTCTCTGAGTGGACAGCAGTCTTCGGGCT	1212
Qy	401	AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
Db	1213	GCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGTGTGTGACATCTTAGCCCTGTTTT	1272
Qy	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1273	GAGCTCTCTTTTGTGCTGCACACAGGTGGCGTTCCTGTGGCAGATGAGAAAGCAGACACGA	1332
Qy	441	ArgGlyThrLysGlyGlyValSerTYRArgProAlaGluValAlaGluThrGlyAla	459
Db	1333	AGGGGAACCAAGGGGGGTGTGAGCTACCGCCACAGCAGAGTAAAGCCGAGACTGGAGCC	1389
RESULT 8			
LOCUS	AR171392	1522 bp	DNA linear PAT 17-DEC-2001
DEFINITION	Sequence 1 from patent US 6297041.		
ACCESSION	AR171392		
VERSION	AR171392.1 GI:17910342		

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Unknown.
Unclassified
1 (bases 1 to 1522)
Zavada, J., Pastorekova, S. and Pastorek, J.
MN gene and protein
Patent: US 6297041-A 1 02-OCT-2001;
Location/Qualifiers
1..1522
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	6.65e-118	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-967-237A-2 (1-459) x AR171392 (1-1522)

QY 1 MetAlaProLeuCySProSerProTyrLeuProLeuLeuIleProAlaProAlaProGly 20

DB 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTGTGATCCCGGCCCTGCTCCAGGC 72

QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40

DB 73 CTCACGTGAACTGCTGCTGCTCACTGCTCTGTAAGCTGCAATCCCGAGAGGTG 132

QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60

DB 133 CCCCAGATGAGAGAGATTCCCTTGGAGAGAGCTCTTGGGGAAGATGACCCCTG 132

QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80

DB 193 GGGGAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGATCCACCCGAGAG 252

QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyGluValPro 100

DB 253 GAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAGTTAACCT 312

QY 101 LysSerGluGluGluGlySerLeuGluGluGluAspLeuProThrValGluAlaProGly 120

DB 313 AATTCAGAAAGAGGGCTCCCTGAATTAGAGATTACTACTGTGAGGGCTCCGGA 372

QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspGlyGluGluAspAspGlnSerHis 140

DB 373 GATCTCTCAAGAACCCCGAATTAATGCCACAGGAGCAAAAGGGGATGACCAAGATCAT 432

QY 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160

DB 433 TGGGCTATGAGGCGAGCCCGCTGGCGGGGTGTCGCCAGCTCCGAGGGCGGCTTC 492

QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180

DB 493 CAGTCCCGGTGATATCCGCCCACTGGCGCTTTCGCCGGCGCTCCGCGCCCTG 552

QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlyGluGluArgLeuArgAsnGlyHis 200

DB 553 GAACCTCTGGGCTTCAGCTCCCGCTCCCAAGTGGCGCTCCCAACCAATGGCCAC 612

QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220

DB 613 AGGTGCAACTGACCTGCTCCCTGGGCTAGAGTGGCTCTGGGCTCCGGGCGGAGTAC 672

QY 221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaAlaGlyArgProGlySerGlnHisThr 240

DB 673 CGGGCTTGACGCTGCACTGCACTGGGGGGCTGCAAGTCTCCGGGCTCGAGACACT 732

QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260

DB 733 GTGGAAGGCCACCGTTCCCTGCGGAGATCCAGTGGTTACCTCAGACCGGCTTGGCC 792

QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280

DB 793 AGAGTTGACAGGCTTGGGGCCCGGAGGGCTGGCGCTGTGGCGGCTTCTGGAG 852

QY 281 GlnGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300

DB 853 GAGGGCCCGGAABAAAACAGTGCCTATGAGCACTTGTGTCTGCTTGGAAAGAAATCGCT 912

QY 301 GlnGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320

DB 913 GAGGAAGGCTCAAGACTCAGTCCAGGACTGAGACTGAGACTGCACTCCGCTCGAC 972

QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340

DB 973 TTCACCGCTACTTCCAAATGAGGGGTCTCTACTACACCGGCTGTGCCAGGGTGTG 1032

QY 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaGlyGlnLeuHisThrLeuSer 360

DB 1033 ATCTGACCTGTGTTTAAACGACAGATGCTGATGTGAAGCAGCTCCACACCTCTCT 1092

QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380

DB 1093 GACACCTGTGGGAGACTGTGTGACTCTCGGCTACACTGAATTCGAGGAGCAGGACCT 1152

QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProAlaAla 400

DB 1153 TTGAATGGCGGAGTGAATTGAGGCTCTCTTCCCTGCTGAGTGAACGACACTCTCGGGCT 1212

QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420

DB 1213 GCTGAGCAAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272

QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440

DB 1273 GGCTCTCTTTTCTGTCAACAGCTGCGCTTCTTGTGAGATGAGAAAGCAGCAGA 1332

QY 441 ArgGlyThrIleGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459

DB 1333 AGGGAAACAAAGGGGTGTGACTACCGCCAGCAGAGGTAGCCAGACTGAGGCC 1389

RESULT 9

AR171563 1522 bp DNA linear PAT 17-DEC-2001

LOCUS Sequence 1 from patent US 6297051.

DEFINITION

AR171563

ACCESSION

AR171563.1 GI:17910513

VERSION

AR171563.1

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1522)

AUTHORS

Zavada, J., Pastorekova, S. and Pastorek, J.

TITLE

MN gene and protein

JOURNAL

Patent: US 6297051-A 1 02-OCT-2001;

FEATURES

Location/Qualifiers

1..1522

source

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	6.65e-118	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-967-237A-2 (1-459) x AR171563 (1-1522)

QY	1	MecAlaProLeuCyPProSerProTriPLeuProLeuLeu1LeProAlaProAlaProGly	20
Db	13	ATGGCTCCCCCTGTGCCCCCAGCCCCCTGGCTCCCTCTGTGATCCCGGCCCCCTGCTCCAGGC	72
QY	21	LeuThrValG1LeuLeuLeuSerLeuLeuLeuLeuMerProAla1AspProG1naGlyLeu	40
Db	73	CTCATCTGTCCAACTGCTGCTGTCTCATCTGTCTTCTGATGCTGTCCATCCCCCAGAGGTTG	132
QY	41	ProArgMetG1nG1uaAspSerProLeuG1yG1ySerSerG1yG1uaAspAspProLeu	60
Db	133	CCCCGGATCAGAGAGGATTTCCCCCTTGGAGGAGGCTCTTCTGAGGAAAGTAGACCACTG	192
QY	61	G1yG1uG1uaAspLeuProSerG1uG1uaAspSerProArgG1uG1uaAspProProG1yG1u	80
Db	193	GGCGAGAGAGACTGTGCCAGTGAAGAGATTCCACCCAGAGAGAGATTCACCCCGGAG	252
QY	81	G1uaAspLeuProG1yG1uG1uaAspLeuProG1yG1uG1uaAspLeuProG1ua1yLysPro	100
Db	253	GAGGATCTACCTGGAGAGAGAGATCTTACTCTGGAGAGAGAGATTTACTTGAAATTAACTT	312
QY	101	LysSerG1uG1uG1uG1ySerLeu1yLysG1uaAspLeuProThrValG1ua1aProG1y	120
Db	313	AAATCAGAAAGAGAGGGCTCCCTCGAAGTTAAGAGATCTTACTGTGTAGGCTCTCCGGA	372
QY	121	AspProG1nG1uProG1naAsnAsnAlaH1sArgAspLysG1uG1yAspAspG1nSerH1s	140
Db	373	GATCTCTCAAGAACCCCGAGATATATGCCACAGGGAACAAAGAGAGATGACCAAGATCAT	432
QY	141	TPATGTYTG1yG1yAspProProTriPProArgValSerProAlaCyAspAlaG1yArgPhe	160
Db	433	TGGCCCTTAAGAGGACACCGCCCTGAGCCCGGGGTCTCCCACTGCTGGCGGACCTTC	492
QY	161	G1nSerProValAsp1LeaArgProG1nLeuAlaAlaPheCyAspProAlaLeuArgProLeu	180
Db	493	CAGTCCCGGTGGATATCCGCCCCCAAGCTGCGCCTTCTGCCCCGACCTCGCCCTCG	552
QY	181	G1uLeuLeuG1yPheG1nLeuProProLeuProG1uLeuArgLeuArgAsnAsnG1yH1s	200
Db	553	GAACCTCTGGGCTTCCAGCTCCCGCGCTCCCAAGACTGGCGCTGGCAACATATGGCCAC	612
QY	201	SerValG1nLeuThrLeuProProG1yLeuG1uMetAlaLeuG1yProG1yAAArg1uTYr	220
Db	613	AGTGTGCAACTACCTGCTGCTCTGGAGTAAAGATGCTCTGTGGTCCCGGAGGAGTAC	672
QY	221	ArgAlaLeuG1nLeuH1sLeuH1sTArgAlaAlaG1yArgProG1ySerG1uH1sThr	240
Db	673	CGGGCTCTGCACTGCTATCTGCACTGGGGGGCTGCAAGTGTCTCGGGCTCGAGACACT	732
QY	241	ValG1uG1yH1sArgPheProAlaG1u1eH1sValValH1sLeuSerThrAlaPheAla	260
Db	733	GTGGAAAGGACCGGTCTTCCTGCGAGATTCAGTGTGTTCACCTCGACACCGCTTGGCC	792
QY	261	ArgValaAspG1ua1aLeuG1yArgProG1yG1yLeuAlaValLeuAlaAlaPheLeuG1u	280
Db	793	AAAGTTGAAGAGAGCCCTGGAGCGCCCGGAGAGGCTGGCCGTGTGTGGCCGCTTTCGAG	852
QY	281	G1uG1yProG1uG1uAsnSerAlaTYrG1uG1nLeuLeuSerArgLeuG1u1eAla	300
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QY	321	PheSerArgTYrPheG1nTYrG1uG1ySerLeuThrThThProProCyAspAlaG1nG1yVal	340
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QY	341	1LeTPTThValPheAsnG1nThrValMetLeuSerAlaLysG1nLeuH1sThrLeuSer	360
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Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis 200
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Qy 221 ArgAlaLeuGlnLeuHisLeuHisLeuGlyValAlaAlaGlyArgProGlySerGlnHisThr 240
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Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
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LOCUS Sequence 71 from Patent EP1439393.
DEFINITION CQ834035
ACCESSION CQ834035
VERSION CQ834035.1 GI:50833640
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Aetle, J.H., Boardman, L.A., Bugart, L.J., Burgess, C.C., Catino, T.J.,
Dwivedi, P., Huntress, M., Johnson, K.A., Lewis, M.E., Maimonis, P.J.,
Myerow, S.H., Brown-Shimer, S.L., Thiagalingam, A., Thibodeau, S.N. and
Molino, G.A.
TITLE Detection methods using TIMP 1 for colon cancer diagnosis
JOURNAL Patent: EP 1439393-A 71 21-JUL-2004;
Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
AND RESEARCH (US)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 6,78e-118 Length: 1552
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Best Local Similarity: 100.00% Mismatches: 0
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Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTACCTGTGAACTGCTGCTGCTCACTGCTCTTCTATGCTCTCCATCCCGAGAGTTG 162
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Qy 181 GluleuLeuGlyPheGlnleuPProProleuPProGlnleuArGVleuArGVAsnGlyHis 200
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Qy 201 SerValGlnleuThrleuPProProGlyleuGlnleuAlaAlaGlyPProGlyArGVGlnTyr 220
Db 643 AGTGTGCAATGACCTCTCTCTGGCTAGAGATGCTGTGGGTCCCGGGCGGGAGTAC 702
Qy 221 ArGVAlaLeuGlnleuHisleuHisleuProGlyAlaAlaGlyArGVProGlySerGlnHisleuThr 240
Db 703 CGGGCTGTGACAGCTCATCTGCATCGGGGGCTGAGGTCTGTCCGGGCTCGAGACACT 762
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RESULT 12
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LOCUS AX330007 1552 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 516 from Patent WO0194629.
ACCESSION AX330007
VERSION AX330007.1 GI:18102985

KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrisan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 516 13-DEC-2001;
FEATURES
source
1. 1552
/organism="Homo sapiens"
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ORIGIN
Alignment Scores:
Pred. No.: 6.78e-118 Length: 1552
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Best Local Similarity: 100.00% Mismatches: 0
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Qy 141 TTPATGTYGTYGTYAASPProProTTPProArGVAlSerProAlaCYAlaGTYArGpHe 160
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DEFINITION Sequence 3116 from Patent WO0194629.
AX332607
VERSION AX332607.1 GI:18123241
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
AUTHORS Horrigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL Patent: WO 0194629-A 3116 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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1. 1552
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Alignment Scores:
Pred. No.: 6,78e-118 Length: 1552
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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LOCUS Sequence 3753 from Patent WO0194629.
DEFINITION AX333244
ACCESSION AX333244.1 GI:18123878
VERSION
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ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
TITLE
Journal Patent: WO 0194629-A 3753 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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Query Match: 100.00% Indels: 0
Gaps: 0
US-09-967-237a-2 (1-459) x AX333244 (1-1552)

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QY 81 GluAspLeuProGlnGlyGluAspLeuProGlnGlyGluAspLeuProGlnValIlyPro 100
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QY 201 SerValGlnLeuThrLeuProProGlnIlyLeuGlnMetAlaLeuGlyProGlyIlyArgIlyThr 220
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QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisValValIleHisLeuSerThrAlaPheAla 260
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Oy	441	ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459
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DEFINITION	Sequence 6683 from Patent WO0194629.		linear
ACCESSION	AX336174		
VERSION	AX336174.1		
KEYWORDS	GI:18126893		
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horriگان, S., Soppet, D.R. and Weaver, Z.		
TITLE	Cancer gene determination and therapeutic screening using signature gene sets		
JOURNAL	Patent: WO 0194629-A 6683 13-DEC-2001;		
FEATURES	Avalon Pharmaceuticals (US)		
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Percent Similarity:	100.00%	Conservative:	0
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US-09-967-237A-2 (1-459) x AX336174 (1-1552)			
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Oy	61	GlyGluGluAspLeuProSerGlnGluAspSerProArgGluGluAspProProGlyGlu	80
Db	223	GGCGAGGAGGATCTGCCAGTGAAGAGATTACCCGAGAGGAGATCCACCCGGAGAG	282
Oy	81	GluAspLeuProGlyGlyGluGluAspLeuProGlyGluAspLeuProGluValLysPro	100
Db	283	GAGATCTACTGAGAGAGAGATCTACTGGAAGAGAGATCTACTGAAGTTAAAGCT	342
Oy	101	LysSerGlnGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly	120
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Oy	121	AspProGlnGluProGlnAspAsnAlaHisArgAspLysGlnGluAspAspGlnSerHis	140
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QY	141	TPRPARGTGYUGIYAAPRPROPTIPRQKRGYVAISERPROAIAQYVAIGIYARGPHE	160
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QY	221	ArgIAIaleuGIInleuHIslleuHIeTRDPIYAIAaIagIYATrProGIYSeGIuHIeTHr	240
Db	703	CGGGCTGTGCAGCTGCATCTGCACITGGGGGGCTGCAGGTCTGCGGGCTCGGAGCACACT	762
QY	241	ValGIuGIYHISATrPheProAIGIuIleHISValYAHISleuSeIThTAlPheAIA	260
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QY	401	AlaGIuPProVAIGInIeuaSnSeCYsIeuaIAaIagIYAAPRIleuAIAleuValIPhe	420
Db	1243	GCTGAGCCAGTCCAGCTGAATCTCTGCTGGCTCTGCTGTGACATCTTAGCCCTGGTTTT	1302
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Db	1303	GGCTCTCTTTTGTCTGCACACAGGCTGCGCTTCTTGTGCAGATGAGAGGACACACAGA	1362
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Search completed: August 20, 2005, 00:09:25
Job time : 6227 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: August 19, 2005, 13:20:06 ; Search time 752 Seconds

(without alignments)
3613.246 Million cell updates/sec

Title: US-09-967-237A-2

Perfect score: 2424
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Scoring table:

BL0SUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2424	100.0	1380	12 ADL70155	ADL70155 Human car
2	2424	100.0	1392	12 ADP54000	ADP54000 Human car
3	2424	100.0	1519	7 ADS73098	ADS73098 Human kid
4	2424	100.0	1522	3 AAT09186	AAT09186 Murli puta
5	2424	100.0	1522	3 AAA16540	AAA16540 Human MN

6	2424	100.0	1522	3 AAA52459	AAA52459 Human MN
7	2424	100.0	1522	12 ADG31413	ADG31413 Human MN
8	2424	100.0	1522	12 ADK41803	ADK41803 Human MN
9	2424	100.0	1552	6 ABL64779	ABL64779 Lung can
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11	2424	100.0	1552	6 ABL65416	ABL65416 Lung can
12	2424	100.0	1552	6 ABL68346	ABL68346 Kidney ca
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14	2424	100.0	1552	8 ABX76124	ABX76124 Lung can
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16	2424	100.0	1552	10 ACC72730	ACC72730 Human can
17	2424	100.0	1552	10 ABZ77284	ABZ77284 Nucleotid
18	2424	100.0	1552	11 ADN39704	ADN39704 Cancer/an
19	2424	100.0	1552	11 ADN38987	ADN38987 Cancer/an
20	2424	100.0	1552	12 ADG31472	ADG31472 Human car
21	2424	100.0	1552	12 ADQ17643	ADQ17643 Human sof
22	2424	100.0	1552	12 ADQ29645	ADQ29645 Human col
23	2424	100.0	1552	13 ADK24713	ADK24713 Breast ca
24	2424	100.0	1552	12 ADQ22315	ADQ22315 Human sof
25	2420	99.8	1552	13 ADQ87399	ADQ87399 Human tum
26	2419	99.8	1833	4 AAH26551	AAH26551 DNA encod
27	2036	84.0	1397	2 AAQ48456	AAQ48456 MN cDNA c
28	1844.5	76.1	1089	12 ADL70159	ADL70159 Human car
29	1600	66.0	978	12 ADL70161	ADL70161 Glu-tagge
30	1596	65.8	1965	12 ADG31474	ADG31474 Murine ca
31	1576	65.0	978	12 ADL70163	ADL70163 Glu-tagge
32	1176.5	48.5	10897	2 AAT09187	AAT09187 Murli puta
33	1176.5	48.5	10898	3 AAA16543	AAA16543 Human MN
34	1176.5	48.5	10898	3 AAA52462	AAA52462 Human MN
35	1176.5	48.5	10898	12 ADG31415	ADG31415 Human MN
36	1176.5	48.5	10898	12 ADK41805	ADK41805 Human MN
37	1176.5	48.5	10898	12 ADP54001	ADP54001 Human car
38	988	40.8	586	12 ADG31473	ADG31473 Human MN
39	763	31.5	540	12 ADL70157	ADL70157 Human car
40	737.5	30.4	6521	10 ADK53977	ADK53977 MNCAS gen
41	737.5	30.4	6521	13 ADK89016	ADK89016 Human gen
42	714	29.5	445	3 AAA16555	AAA16555 Human MN
43	714	29.5	445	3 AAA52474	AAA52474 Human MN
44	666	27.5	579	13 ADQ50263	ADQ50263 Novel can
45	629	25.9	1401	3 AAA16576	AAA16576 Human MN

ALIGNMENTS

RESULT 1	
ID ADL70155	ADL70155 standard; cDNA; 1380 BP.
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XX	ADL70155;
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DT	20-MAY-2004 (first entry)
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DE	Human carbonic anhydrase isozyme CA IX coding sequence.
XX	
KW	Human; carbonic anhydrase; tumour; antigen; cytosolic; gene; ss.
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OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
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FT	1..110
FT	/*tag= a
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PN	MO2004017923-A2.
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PD	04-MAR-2004.
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PF	25-AUG-2003; 2003WO-US026612.
XX	

PR 23-AUG-2002; 2002US-040577P.
PR 22-AUG-2003; 2003US-00646934.
XX
PA (CHIR) CHIRON CORP.
XX
PI Wong J, Winter J, Lalehzadeh G, Warne R;
XX
DR WPI; 2004-226730/21.
DR P-PSDB; ADL70156.
XX
PT Identifying an agent capable of inhibiting carbonic anhydrase (CA)
PT activity of CA IX polypeptide for treating cancers, comprises combining a
PT test agent with a cell expressing CA IX and assessing CA inhibitory
PT activity of the test agent.
XX

PS Example 6; SEQ ID NO 1; 82pp; English.

XX The present sequence is the coding sequence for human carbonic anhydrase
CC 18ozyme IX (CA IX), an N-glycosylated membrane-associated glycoprotein
CC also known as the MN or G250 tumour-associated antigen. The invention
CC relates to compositions and methods useful in inhibiting CA IX-
CC preneoplastic or neoplastic cells. The inhibitors are especially
CC antagonistic anti-CA IX antibodies and other inhibitory agents that
CC target the carbonic anhydrase activity of CA IX on these cells. The
CC antibodies, or their antigen-binding fragments, are specifically reactive
CC with an inhibitory epitope of CA IX. Screening assays for identifying
CC such inhibitory agents are provided. The antibodies, their antigen-
CC binding fragments, and other inhibitory agents are useful in the
CC treatment of cancers characterised by the expression of CA IX, such as:
CC head and neck cancers; gynaecological cancers including ovarian,
CC cervical, vaginal, endometrial and vulval cancers as well as
CC gynaecological precancerous conditions such as metaplastic cervical
CC tissues and condylomas; gastrointestinal cancers such as stomach, colon
CC and oesophageal cancers; urinary tract cancer such as bladder and kidney
CC cancers; skin cancer; liver cancer; prostate cancer; lung cancer; and
CC breast cancer.
XX

SQ Sequence 1380 BP; 257 A; 428 C; 420 G; 275 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1 47e-130	Length:	1380
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-967-237a-2 (1-459) x ADL70155 (1-1380)

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QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspProLeu 60
Db 121 CCCCGGATGCGAGAGATTCCCTTGGAGAGAGCTCTTGGAGAGAGTACCCACTG 180
QY 61 GlyGlnGluAspLeuProSerGlyGluAspSerProArgGlnGluAspProProGlyGlu 80
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Db 241 GAGGATCTACTCGAGAGAGAGATCTCTGAGAGAGAGATCTCACTGAAGTTAAACCT 300
QY 101 LysSerGlnGluGlySerLeuLeuLeuGlnAspLeuProThrValGlnAlaProGly 120
Db 301 AATTCAGAAAGAGGGCTCCCTGAAGTTAGAGGATCTACTCTGTGAGGCTCTGGA 360

QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspArgGlnSerHis 140
Db 361 GATCTCTCAAGAACCCCGAATATATGCCACAGAGGACAAAGAGGATGACAGAGTCA 420
QY 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 421 TGGCGCTATGAGAGCGACCCGCTGGCCCGGGGTGTCCCACTGCGGGCCGCTTC 480
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuAspProLeu 180
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QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1141 TTAATGGCGGAGATTTGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
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QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrArgVala 459
Db 1321 AGGGAACCAAGGGGTGTGAGCTTACGCCCAAGCAAGGTACCCAGACTGAGGCC 1377
RESULT 2
ADP54000
ID ADP54000 standard; DNA; 1392 BP.
XX
AC ADP54000;

[illegible][illegible]

Qy 341 ILeTrpThrValPheAenGlnThrValMetLeuSerAlaIysGlnLeuHisThrLeuSer 360
Cc 1033 ATCTGGAGCTGTGTTTAAACAGACAGTATGCTAGTCTTAAGACGCTCCACACCTCTCT 1092
Db 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Qy 1093 GACACCTGTGGGAGACTGGTGACTCTCGGCTACAGCTGAACCTCCAGAGCAGCAGCCT 1152
Db 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Qy 1153 TTGATGAGGAGATGATTGAGCTCTCTCTCTGAGTGAAGACAGCAGCTCTGGGCT 1212
Db 401 AlaGluProValGlnLeuAsnSerCysLeuAlaIleGlyAspIleLeuAlaLeuValPhe 420
Qy 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGTCGTCGTCGTCGCTGCTTTT 1272
Db 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Qy 1273 GGCTCTCTTTTGTCTGTCCACAGCGCTGCTCTCTCTGTGAGATGAGAGCAGCAGCA 1332
Qy 441 ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGGAACAAAGGGGTGTGAGCTACCGCCAGCAGAGTGAAGCTGAGGCC 1389
RESULT 3
ADS73098
ID ADS73098 standard; cDNA; 1519 BP.
XX
AC ADS73098;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human kidney tumour specific cDNA, SEQ ID 1695.
XX
KW Human; ss; kidney tumour; kidney cancer; cytostatic; gene therapy;
XX
KW T-cell; immune response.
XX
OS Homo sapiens.
XX
PN US2003109434-A1.
XX
PN 12-JUN-2003.
XX
PF 19-MAR-2002; 2002US-00102524.
XX
PF 19-MAR-2001; 2001US-0277245P.
XX
PR 21-DEC-2001; 2001US-0343340P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Mannion J, Gaiger A, Gordon B, Harlocker SL;
XX
XX WPI; 2002-759855/82.
XX
PT New isolated polynucleotides and polypeptides, useful for detecting the
PT presence of, and treating cancer, particularly kidney cancer by
PT stimulating T-cells specific for a tumor protein, and stimulating immune
PT response in a patient.
XX
PS Claim 1; SEQ ID NO 1695; 78BP; English.
XX
XX The invention relates to a new isolated polynucleotide (a Human kidney
CC tumour specific cDNA) comprising any one of the 1855 sequences identified
CC in the specification (or their complements, degenerate variants,
CC sequences consisting of at least 20 contiguous residues them, sequences
CC that hybridize to them under highly stringent conditions or sequences
CC having at least 75 or 90% sequence identity to the 1855 sequences. Also
CC included are detecting/determining the presence of cancer in a patient,
CC stimulating an immune response in a patient; treating kidney cancer in a
CC patient, an isolated polypeptide encoded by one of the 1855 sequences, an
CC expression vector comprising the polynucleotide operably linked to an
CC expression control sequence, a host cell transformed/transfected with the

CC vector, an isolated antibody (or its antigen-binding fragment) that
CC specifically binds to the protein, a fusion protein comprising at least
CC one the proteins, stimulating and/or expanding T-cells specific for a
CC tumour protein, an isolated T-cell population comprising the T-cells, a
CC composition comprising a first component (such as a carrier or
CC immunostimulant) and a second component (comprising one of the
CC polynucleotides, the polypeptides, an antibody, T-cell or an antigen-
CC presenting cell that expresses the polynucleotide) and a diagnostic kit
CC comprising at least one of the oligonucleotides, or at least one antibody
CC and a detection reagent comprising a reporter group. The polynucleotides,
CC polypeptides, antibodies and antigen-presenting cells are useful for
CC detecting the presence of, and treating cancer, particularly kidney
CC cancer by stimulating and/or expanding T-cells specific for a tumour
CC protein, and stimulating immune response in a patient. The present
CC sequence is one of the Human kidney tumour specific cDNAs. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docid=20030109434.
XX
SQ Sequence 1519 BP; 296 A; 456 C; 453 G; 314 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,62e-130 Length: 1519
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0
US-09-967-237A-2 (1-459) X ADS73098 (1-1519)
Qy 1 MetAlaProLeuCysProSerProTyrPLeuProLeuLeuIleProAlaProGly 20
Db 10 ATGGCTCCCTGAGCCCAAGCCCTCGCTGCTGATCCCGGCTCTCCAGGC 69
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 70 CTCACGTGTCAATGCTGTGCTGTCACGCTGCTCTATGCTGTCCATCCCAAGAGTTG 129
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 130 CCCCAGATCGAGAGATTCCTCCCTTGGAGAGGCTCTTCTGGGAAGATGCCACTG 189
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 190 GCGAGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGATCCACCGGAGAG 249
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValLysPro 100
Db 250 GAGGATCTACCTTGAAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAGTTAAGCT 309
Qy 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 310 AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACCTGTTAGGCTCTCGGA 369
Qy 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGluAspAspGlnSerHis 140
Db 370 GATCCTCAAGAAACCCAGAAATATGCCACAGGAGCAAAAGAGGATGACAGATCAT 429
Qy 141 ThrArgTyrGlyGlyAspProProTyrProArgValSerProAlaGlyValGlyArgPhe 160
Db 430 TGGGCTTATGAGAGCAACCGCTGCGCGGGGTCTCCCACTGCGGGGCGGCTTC 489
Qy 161 GluSerProValAspIleArgProGlnLeuAlaIlePheCysProAlaLeuArgProLeu 180
Db 490 CAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTCTGCGGCGCTCCGCCCTC 549
Qy 181 GlyLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnArgHis 200
Db 550 GAACCTCTGGGCTTCAGCTCCGCGCTCCGGAATCGAGCTGCGGCAACAATGCGCAC 609
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220

Db 610 AGTGTCACTGACCTGCTCTCTGAGATGAGTCTGAGTCTGAGGCGGAGTAC 669
Qy 221 ATGATALEUAGLNUHISLEUHISTRPGLYAALAGLYARGPROGLYSEGLUHSIHR 240
Db 670 CGGGCTCTGACAGCTGATCTGACGAGGAGGCTGAGGCTGCGGCTCGAGACACT 729
Qy 241 VALGUGLYHISARGPHEPROAGLUTLEHISVALHISLEUSERTHRALAPHEA 260
Db 730 GTGAGAGCCACCGTTTCCCTGCGAGATCCAGTGTCTCACTCAGACCCGCTTTGCC 789
Qy 261 ARGVALAPRGUJALEUGLYARGPROGLYSEGLUJALEUJALAPHELEUGLU 280
Db 790 AGAGTTGACGAGGCTTGGGGGCGCGGAGGCTGCGCGGTGTGGCCCTTTCTGGAG 849
Qy 281 GLUGLYPROGLUGLUANSERLARYTGLUINLEULEUSERARGLEUGLUJLEA 300
Db 850 GAGGCGCCGGAAGAAACAGTGCCTATGACAGTGTCTGCTCGCTTGAAGAAATCGCT 909
Qy 301 GLUGLYSERGLUTHRGLINVALPROGLYLEUAPLIESERLALALEUENPROSERASP 320
Db 910 GAGAGAGCTCAGAGACTCAGGCTCCAGAGACTGACATHTCTGACTCTGCTGCTGAC 969
Qy 321 PHESEARGLYRPHGLINTYRGLUGLYSERLEUTHRTHTPROPCYALAGLNGLYA 340
Db 970 TTCAGCCGCTACTTCCATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGTCT 1029
Qy 341 ILETPTHTVALPHEAENGINTHRVALMETLEUSERALALYSGLINLEUHSITHRLEUSER 360
Db 1030 ATCTGAGACTGTGTTTACACAGACAGTGAATGCTGAGTGTGTAAGCACCTCCACCTCTCT 1089
Qy 361 ASPHTLEUTHRTPGLYPROGLYASPSERARGLEUGLINLEUANSPPHEARGALATHRGINPRO 380
Db 1090 GACACCCCTGTGGGACCTGTGACCTCTGCGCTACGCTGAACTCCGAGCAGCAGGCT 1149
Qy 381 LEUANGLYARGVALILEGLUALASERPHEPROAGLYVALASPSERSETPROARGA 400
Db 1150 TTGAATGGGCGAGTATGAGGCTCTTCCCTGTGAGTGAACAGACAGTCTCTGGGCT 1209
Qy 401 ALAAGUPROVALGINLEUANSERCYALEUJALAGLYAPLILEUJALALEUVALPHE 420
Db 1210 GCTAGGCCAGTCCAGCTAAATTCCTGCTGCTGTGACATCTAGCCCTGTGTTTTT 1269
Qy 421 GLYLEULEUPHEALAVALTHSERVALALAPHELEUVALGINMETARGARGINHSIARG 440
Db 1270 GGCCTCTTTTTCCTGTACACAGGCTCCGCTTCTCTGTGCAATGAGAAGCAGACAGA 1329
Qy 441 ARGGLYTHRILYSGLYVALISERTYRARGPROAGLUJALAGLUTHRGLYA 459
Db 1330 AGGGGAACCAAGGGGTGTGAGTACCGCCAGAGAGTACCGAGACTGAGGCC 1386

RESULT 4
AAT09186
ID AAT09186 standard; cDNA, 1522 BP.
XX
AC AAT09186;
XX
DT 25-MAR-2003 (revised)
DT 19-AUG-1996 (first entry)
XX
DE MUTU putative oncogene MN cDNA.
XX
KM MUTU; endogenous; cellular component; MN; Hela cell; diagnosis;
KM lymphocytic choriomeningitis virus; LCMV; putative oncogene; treatment;
KM neoplastic; pre-neoplastic; disease; anticense therapy; antibody;
KM vaccine; vertebrate; immunisation; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 13..1392
XX /*tag= a
FN ,M09534650-A2.

XX 21-DEC-1995.
PD 15-JUN-1995; 95WO-US007628.
XX 15-JUN-1994; 94US-00260190.
XX 07-JUN-1995; 95US-00477504.
PR 07-JUN-1995; 95US-00481658.
PR 07-JUN-1995; 95US-00485049.
PR 07-JUN-1995; 95US-00485862.
PR 07-JUN-1995; 95US-00485863.
PR 07-JUN-1995; 95US-00486756.
PR 07-JUN-1995; 95US-00487077.
XX
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
XX
PI Zavada J, Pastorekova S, Pastorek J;
XX MPI, 1996-049679/05.
DR P-P8DB; AAR88058.
XX
PT MN gene, protein and nucleic acid fragments - used as primers and probes
PT in the detection of MN antigens and antibodies, and in the treatment of
PT (pre)neoplastic disease.
XX
PS Claim 1; Fig 1; 102pp; English.
XX
CC The present sequence is the full length Mutu endogenous cellular
CC component, MN, cDNA clone, which was isolated from lymphocytic
CC choriomeningitis virus (LCMV) infected Hela cells. Persistent LCMV, the
CC exogenous Mutu transmissible agent (MX), infection increases the
CC expression level of the MN gene. MN is a putative oncogene, and can
CC therefore be used in the development of prods. for the diagnosis and
CC treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be
CC treated using DNA antisense to MN transcribed mRNA, anti-MN protein
CC antibodies can be used for the diagnosis NP or pre-NP diseases and a
CC vaccine contg. immunogenic amounts of the MN protein can be used to
CC immunise a vertebrate against a NP disease associated with MN antigen
CC expression. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
XX

Alignment Scores:
Pred. No.: 1,62e-130 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-967-237A-2 (1-459) x AAT09186 (1-1522)
Qy 1 MetAlaproleuCyProSerProTrpLeuProleuLeuJleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCTGCCAGCCCTGAGCTCCTGTGTGATCCGCGCCCTGCTCCAGGC 72
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGCAACAGCTGCTGCTCTCACTGCTGCTTGTGATGCTGTCATCCCAAGGTTG 132
Qy 41 ProArgMetGlnJuaPserProLeuGlyGlyGlySerSerGlyJuaPAspProLeu 60
Db 133 CCCCAGATCGAGAGATTCCTCCCTTGGAGAGAGGCTCTTGGGAGAAATGATCCACTG 192
Qy 61 GlyGlnJuaPLeuProSerGlnJuaPserProArgGlnJuaPProProGlyGlu 80
Db 193 GCGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCGAGAG 252
Qy 81 GluaPLeuProGlyGlnJuaPLeuProGlyGlnJuaPLeuProGlnValValPro 100
Db 253 GAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAGTTAAGCT 312

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QY 101 LysSerGluGluGluGluSerLeuLeuGluAspLeuProThraValGluAlaProGly 120
DB 313 AAATCAAGAAAGAGGGCTCCCTGAAGTATGAGGATCTACTGTTGAGGCTCTCGA 372
QY 121 AspProGluGluProGluAsnAsnAlaHisArgAspLeuGluGluAspAspGlnSerHis 140
DB 373 GATCTCTCAAAACCCCAAGATTAATGCCCACAGAGGAAAGAGGGGTGACCAAGATCAT 432
QY 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
DB 433 TGGCGCTATGAGGCGACCCGCCCTGGCCGCCGGGTGTCCCAAGCTTCGCGGCGCGTTTC 492
QY 161 GlnSerProValAsp11eArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 493 CAGTCCCGCGGTGATATCCCGCCCCAGCTGCGCGCTTCTGCCCCGCGCCCTCCCTG 552
QY 181 GluLeuLeuGlyPheGluLeuProProLeuProGluLeuArgPheArgAsnAsnGlyHis 200
DB 553 GAACTCTGGGCTTCACAGCTCCGCGCGCTCCAGAACTGCGCTGCGCAACAAATGGCCAC 612
QY 201 SerValGlnLeuThraLeuProProGlyLeuGluLueAlaLeuGlyProGlyArgGlyTyr 220
DB 613 AGGTGTCAATGACCCCTGCTCCGCGCTAGAGATGCTCTGGGTCCCGGCGGAGTAC 672
QY 221 ArgAlaLeuGluLeuHisLeuHisSerGlyValAlaAlaGlyArgProGlySerGluHisThr 240
DB 673 CGGCGCTCTGAGCTGATCTGCACTGGGGGGCTGCAAGTGTCTCGCGGCTCGAGCACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluAlaHisValValHisSerSerThrAlaPheAla 260
DB 733 GTGGAAAGGCCACCGTTTCCCTGCGAGATCCAGTGTCTACTCTCAGACCCGCTTTGCC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
DB 793 AGAGTTGACAGGCGCTTGGGGCGCGCGAGGCGCTGGCGGTGTGGCGGCTTTCTGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGluLeuLeuSerArgLeuGluGluAla 300
DB 853 GAGGGCCCGGAAACAAACAGTGTCTATGACAGTGTCTGCTGCTGGAAAGAACTGCT 912
QY 301 GluGluGlySerGluThraGluValProGlyLeuAsp11eSerAlaLeuLeuProSerAsp 330
DB 913 GAGGAAGGCTCAAGACTCAGGTCCAGACTGCACTGATCTGCTCCTGCTCTGAC 972
QY 332 PheSerArgTyrPheGlnTyrGluGlySerLeuThraProProCysAlaGlnGlyVal 340
DB 973 TTCAGCCGCTACTTCCAAATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTTC 1032
QY 341 IleTyrThrValPheAsnGlnThraValMetLeuSerAlaGlyGlnLeuHisSerThrLeuSer 360
DB 1033 ATCTGACCTGTGTTTAAACGACAGATGATCTGATGCTAAGACGCTCCACACCTCTCT 1092
QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGluLeuAsnPheArgAlaThrGlnPro 380
DB 1093 GAAACCTGTGGGGAAGCTGTGACTCTCGGCTACAGCTGAACCTCCAGGGAAGACGCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB 1153 TTGAATGGGCGAGTGTGAGGCTCTCTCCCTGCTGAGTGAACAGAGACTCTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAsp11eLeuAlaLeuValPhe 420
DB 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGTGTGTACATCTCAGCCCTGGTTTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
DB 1273 GCGCTCTTTTCTGTGTGACCAAGCTGCGCTTCTGTGTGACATGAGAGGACGACACA 1332
QY 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
DB 1333 AGGGAAACCAAGAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCAGAGACTGAGGCC 1389
```

RESULT 5

```
AA16540
ID AA16540 standard; cDNA; 1522 BP.
XX
AC AA16540;
XX
DT 16-JUN-2000 (first entry)
DE
XX Human MN protein encoding cDNA SEQ ID NO:1.
XX
XX Human: MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KM MN/CA IX isoenzyme; ds.
XX
XX Homo sapiens.
OS
XX US6027887-A.
PN
XX
PD 22-FEB-2000.
XX
XX
XX 24-JAN-1997; 97US-00787739.
XX
XX 21-OCT-1992; 92US-00964589.
PR 30-DEC-1993; 93US-00177093.
PR 15-JUN-1994; 94US-00260190.
PR 07-JUN-1995; 95US-00477504.
PR 07-JUN-1995; 95US-00481658.
PR 07-JUN-1995; 95US-00485049.
PR 07-JUN-1995; 95US-00485862.
PR 07-JUN-1995; 95US-00485863.
PR 07-JUN-1995; 95US-00486756.
PR 07-JUN-1995; 95US-00487077.
XX
XX (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
PA
XX Pastorek J, Zavada J, Pastorekova S;
PI
XX WPI; 2000-194827/17.
DR
XX P-PDB; AAY53228.
XX
XX PT Nucleic acid based assay for diagnosing a wide variety of
PT preneoplastic/neoplastic disease comprises screening for the presence of
PT abnormal MN gene expression in a vertebrate.
XX
XX Claim 1; Fig 1; 87PB; English.
XX
XX PS The present invention describes a method of screening for
XX preneoplastic/neoplastic disease. The method comprises: (1) determining
XX whether abnormal MN gene expression is present in a vertebrate; and (2)
XX if abnormal MN gene expression is determined to be present in the
XX vertebrate, determining that the vertebrate has a significant risk of
XX having preneoplastic/neoplastic disease. The MN gene is an oncogene and
XX encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
XX protein is a tumour associated carbonic anhydrase isoenzyme. The method
XX is used for detecting a wide variety of preneoplastic/neoplastic diseases
XX in a vertebrate, preferably a human. The disease detected is mammary,
XX bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
XX vaginal, vulvar, prostate, liver, lung, skin, thyroid, pancreatic,
XX testicular, brain, head and neck, mesodermal, gallbladder, rectal,
XX duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
XX mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
XX mucosa, pancreatic duct epithelium or liver duct epithelium
XX CC preneoplastic/neoplastic disease. AA16540 to AA16617 and AAY53228 to
XX CC AAY53245 represent sequences used in the exemplification of the present
XX CC invention
XX
XX SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,62e-130 Length: 1522
XX Score: 2424.00 Matches: 459
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
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DB: 3 Gaps: 0
US-09-967-237a-2 (1-459) x AA16540 (1-1522)
QY 1 MetalaproleuCyepSerProTtrleuProleuLeuileProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGGCCCGAGCCCTGGCTCCCTGTGGATCCCGGCCCTCTCCAGGC 72
QY 21 LeuTrValGlnLeuLeuSerleuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACTGGCAACCTGCTGTCACTGCTTCTGAATGCTGTCCATCCCGAGGTTG 132
QY 41 ProArgMetGlnGluAaspSerProleuGlyGlySerSerGlyGluAaspProleu 60
Db 133 CCGCGAGTGCAGAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAGAGATCCCATCTG 192
QY 61 GlyGluGluAaspLeuProSerGlyGluAaspSerProArgGluGluAaspProGlyGlu 80
Db 193 GCGGAGAGAGATCTCCAGTGAAGAGATTCACCAGAGAGAGATCCACCCGAGAG 252
QY 81 GluAaspLeuProGlyGlyGluAaspLeuProGlyGlyGluAaspLeuProGlyValLysPro 100
Db 253 GAGATCTCACTCGAGAGAGAGATCTACCTGAGAGAGATCTCACTGAAGTTAAGCT 312
QY 101 LysSerGluGluGlySerLeuLysLeuGluAaspLeuProThrValGlnAAlaProGly 120
Db 313 AAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTAATCTTGAAGCTCTTGA 372
QY 121 AaspProGluGluProGluAaspAaspAAlaHisArgAaspLysGlyGluAaspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCAAGATATATGCCACAGAGCAAAAGAGGATGACCAAGTCA 432
QY 141 TTPATGTYTGYGlyAaspProProTtrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGGCTATGAGAGGAGCCCGCTGGCCCGGAGTGTCCCAAGCTTGGCGGCGCTTC 492
QY 161 GlnSerProValAaspArgProGlnLeuAAlaPheCysProAlaLeuArgProleu 180
Db 493 CAGTCCCGGTGGATATCCGCCCAAGCTCCGCGCTTCTGCGCGCCCTGGCGCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProleuProGluLeuArgLeuArgAaspGlnHis 200
Db 553 GAATCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTCGCAACAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlnLys 220
Db 613 AGTGTGAACCTGACCTCTCTGGGCTGAGAGAGCTCTGGGCTCCGGGGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CCGGCTCTGACGCTGATCTGCACTGGGGGGCTGCAAGTCTCGGGCTCGAGCAACT 732
QY 241 ValGluGlyHisArgPheProAlaGlnLeuHisValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGAGATCCAGTTCACCTCAGCAACCGCTTTGCC 792
QY 261 ArgValAaspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln 280
Db 793 AGAGTTGACGAGGCTTGGGGGCGCGGAGAGCTGGCGGTGGCCGCTTCTGGAG 852
QY 281 GlyGlyProGluGluAaspSerAlaTrpGluGlnLeuLeuSerArgLeuGlnLysAla 300
Db 853 GAGGCGCCGAGAGAGAGAGTGCCTATAGCACTTGTCTCTCGCTTGGAGAGAAATCCCT 912
QY 301 GlyGluGlySerGluThrGlnValProGlyLeuAaspLysSerAlaLeuLeuProSerAasp 320
Db 913 GAGAGAGGCTCAGAGACTCAGGTTCCAGAGACTGAGCATATCTGCACTCGGCTCTGAC 972
QY 321 PheSerArgGlyTrpPheGlnTrpGlyGlySerLeuThrTrpProProCysAlaGlnLysVal 340
Db 973 TTTCAGCCCTACTTCTCAATATGAGGGGCTCTGATACACCGCCCTGTGGCCAGGGTCTC 1032
QY 341 IleTrpThrValPheAaspGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360

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Db 1033 ATCTGACCTGTGTTTAACCAAGCAGTGAATGCTGAGTGTAAAGCACTCCAGCCCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAaspSerArgLeuGlnLeuAaspPheArgAlaThrGlnPro 380
Db 1093 GACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTTCCGAGCGCAGGCT 1152
QY 381 LeuAaspGlyArgValIleGluAlaSerPheProAlaGlyValAaspSerProArgAla 400
Db 1153 TTGAATGGCCAGATGATTAAGGCTCTTCCCTGCTGAGAGTGAACAGACATGCTCGGCT 1212
QY 401 AlaGluProValGlnLeuAaspSerCysLeuAlaAlaGlyAaspLysLeuAlaValPhe 420
Db 1213 GCTAGCAGAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTCTTTTGGCTGTGACCAAGCGCTCCGTTCTTGTGCAAGATGAGAAAGCAGACAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTrpArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAGACCAAGGGGGTGTAGCTACCGCCAGCAGAGTACCGAGACTGAGGCC 1389

RESULT 6
AAAS2459
ID AAAS2459 standard; cDNA; 1522 BP.
AC AAAS2459;
DE 25-SEP-2000 (first entry)
XX Human MN cDNA.
XX MN protein; tumour associated cell adhesion molecule; oncoprotein;
XX proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
XX abnormal expression; neoplastic disease; cancer; gene therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 13..1392
FT FT /*tag= a
FT FT /product= "Human MN protein"
XX
XX MO2000024913-A2.
XX
XX 04-MAY-2000.
XX
XX 22-OCT-1999; 99MO-US024879.
XX
XX 23-OCT-1998; 98US-00177776.
XX
XX 23-OCT-1998; 98US-00178115.
XX
XX (FARB ) BAYER CORP.
XX PA (VIRO-) INST VIROLOGY.
XX
XX Zavada J, Pastorekova S, Pastorek J;
XX WPI; 2000-350752/30.
XX
XX P-PSDB; AAB03005.
XX
XX A molecule which specifically binds to a site on MN protein (oncoprotein)
XX and prevents adhesion of vertebrate cells to the protein, useful for
XX treating preneoplastic or neoplastic diseases such as cancer.
XX
XX Example 1; Fig 1A-C; 154p; English.
XX
XX The invention relates to the inhibition of cell adhesion mediated by the
XX MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
XX protein). The MN protein is a tumour-associated adhesion molecule which
XX comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
XX protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
XX Abnormal expression of the MN protein is associated with tumorigenicity.
XX

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CC The invention encompasses molecules (e.g., proteins and peptides) which
CC which specifically bind to a site on the MN protein, thereby preventing
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC also encompasses MN proteins or MN protein fragments which can be added
CC to the extracellular environment to prevent the adhesion of vertebrate
CC cells to each other. The invention also relates to the identification of
CC the binding site of the MN protein and to a method of identifying a site
CC on an MN protein to which cells adhere, comprising testing a series of
CC overlapping peptides from the protein in a cell adhesion assay. The
CC invention encompasses a vector comprising an expression control sequence
CC operatively linked to a nucleic acid encoding the variable domain of a
CC MN-specific antibody, where the domains are separated by a flexible
CC linker peptide (Aa503035) and the vector inhibits the growth of a
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC protein. The invention also encompasses a vector comprising a nucleic
CC acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC gene promoter (Aa52473). MN proteins and peptides, MN-binding proteins
CC and peptides, and expression vectors encoding such proteins and peptides
CC are useful for treating patients with preneoplastic or neoplastic disease
CC (e.g., cancers) associated with or characterised by abnormal MN
CC expression. The present sequence represents cDNA encoding the human MN
CC protein

XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1 62e-130	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-967-237a-2 (1-459) x Aa52459 (1-1522)

QY 1 MetAlaProLeuCySPSePrProTPrLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCTCTGTGTGATCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTACAGTGTGCACTGCTGTGTCACTGCTCTGTGTGCTGTCCATCCCAAGAGTTG 132
QY 41 ProArgMetGlnLeuAspSerProLeuGlyGlySerSerGlyLeuAspAspProLeu 60
Db 133 CCCCAGATGAGAGGATTTCCCTTGGAGAGGCTCTTCTGGGAAAGTACCCACTG 132
QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGly 80
Db 193 GCGAGAGGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGATTCACCCGGAGAG 252
QY 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyValHisPro 100
Db 253 GAGAGATCTACCTGAGAGAGAGATTTACCTGAGAGAGAGATTTACCTGAAGTTAAACCT 312
QY 101 LysSerGlnGlnGlnGlnSerLeuLeuGlnAspLeuProThrValGlnAlaProGly 120
Db 313 AAATCAGAAAGAGGCTCCCTGAAGTTAGAGATTTACTTACTGTGAGCTCTCGGA 372
QY 121 AspProGlnGlnProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
Db 373 GATCTCAAGAACCCCGAATTAATGCCCACAGGGAACAAAGAGGATGACCAAGATCAT 432
QY 141 ThrArgTyrGlyLysAspProProTPrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGAGAGCGAGCCCGCTGGCCCGGGGTGTCCCTACCGTGGCGGCGGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCCGGAGCTGCGCCCTTCTGCGCGGCTGCGCCCTG 552

QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnArgHis 200
Db 553 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGGCAACAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGGTGCACATGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCGGGGCGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisIleuHisIleuHisIleuHisIleuHisIleuHisIleuHis 240
Db 673 CGGGCTCTGAGCTGATCTGCACTGGGGGCTGAGAGTGTGTCGGGCTGGAGCACACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnLeuHisValHisIleuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGAGATCCAGTGGTTTCACTCCAGCACCGGCTTGGC 792
QY 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGGCCCGGAGGCTGGCCGTGTGGCCGCTTCTGGAG 852
QY 281 GlyGlyProGlnGlnLeuAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnLeuAla 300
Db 853 GAGGCGCCGGAAGAAACAGTGCCTATGAGCACTTGTCTGCTTGGAAAGAAATGCT 912
QY 301 GlyGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGTCCAGAGACTGAGACATATCTCCTGCTGCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrProProCysAlaGlnGlyVal 340
Db 973 TTCAAGCGCTACTTCCAAATGAGGGGTCTCTGACTACACGCGCTGTGCGAGGGTGT 1032
QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisIleuSer 360
Db 1033 ATCTGACGTGTGTTTAAACAGACAGTGAATCTGAGTGTACGACGCTCCACCTCTCT 1092
QY 361 AspThrLeuTPrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGACTGTGTGACTCTCGGCTACAGCTGAATTCGAGGAGGAGCCCT 1152
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGAGTGAATTTAGAGCTCTCTTCTCTGCTGAGTGAACAGCACTCTCGGGCT 1212
QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTCTTTTCTCTGACACAGCTGCGCTTCTTGTGCAAGTGAAGAGGAGCAGACA 1332
QY 441 ArgGlyThrIleGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
Db 1333 AGGGAACCAAGAGGGGTGTGAGCTACCGCCACAGAGGTACCGAGACTGAGGCC 1389

RESULT 7
ADG31413
ID ADG31413 standard; cDNA, 1522 BP.
XX
AC ADG31413;
DT 26-FEB-2004 (first entry)
XX
DE Human MN cDNA, Segid 1.
XX
KW human; gene; ss; monoclonal antibody; MN/CA IX; MN; oncogene;
KW carbonic anhydrase 9; CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/G250;
KW neoplastic tumour; cyostatic; cancer; tumour therapy;
KW anti-tumour vaccine.
XX
OS Homo sapiens.
XX

PN W02003100029-A2.
XX 04-DEC-2003.
XX 22-FEB-2003; 2003WO-US0005136.
XX 23-MAY-2002; 2002US-0383068P.
PR 05-DEC-2002; 2002US-0431499P.
XX (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
PI Pastorek J, Pastorekova S, Zatoricova M, Zavada J, Ortova Gut M;
XX WPI; 2004-035136/03.
DR P-PSDB; ADG31414.
XX
PT New monoclonal antibody generated from MN/CA IX-deficient mice, where the
PT antibody binds specifically to human tumor-associated cell adhesion
PT protein MN/CA IX or polypeptide, useful for diagnosing, prognosing or
PT treating cancer.
PS Disclosure; SEQ ID NO 1; 156bp; English.
XX
XX This invention relates to a novel monoclonal antibody identified as the
CC MN/CA IX specific antibody prepared in knockout mice (CA IX deficient
CC mice). Specifically, this antibody is directed towards the MN gene, a
CC cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or
CC MN/CA9, which encodes the MN protein that is also known as the MN/CA IX
CC isoenzyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The
CC present invention describes the generation of this monoclonal antibody,
CC and immunoreactive fragments thereof, which are directed against non-
CC immunodominant epitopes on the CA IX extracellular domain. As such, this
CC antibody can be useful diagnostically as a marker for preneoplastic/
CC neoplastic tumors, immunodetection methods and immunotargeting
CC approaches. Accordingly, compositions exhibit cytostatic activity and are
CC useful in the diagnosis, prognosis and treatment of various cancers
CC including breast, bladder or lung cancer, in tumor therapy and in anti-
CC tumor vaccination. This polynucleotide sequence is the human MN cDNA of
CC the invention.
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1.62e-130 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 12 Indels: 0
Gaps: 0
US-09-967-237A-2 (1-459) x ADG31413 (1-1522)
QY 1 MetAlaProLeuCySProSerProTyrLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGCTGCTCCCGAGCCCTGCTGCTGTTGATCCGCGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACCTGCAACAGCTGCTGCTCACTGCTGCTTCGATGCTGCATCCCAAGAGGTG 132
QY 41 ProArgMetGlnGlnuAspSerProLeuGlyGlyGlySerSerGlyGlyuAspAspProLeu 60
Db 133 CCCCAGGAGGAGGAGGATTCCTCCCTTGAGAGAGGCTTCTTGAGAGAGATGACCCACTG 192
QY 61 GlyGlnGlnuAspLeuProSerGlnGlnuAspSerProArgGlnGlnuAspProGlyGln 80
Db 193 GGGCAGGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAGATCCACCGGAGAG 252
QY 81 GlnuAspLeuProGlyGlnGlnuAspLeuProGlyGlnGlnuAspLeuProGlnValValPro 100
Db 253 GAGGATCTACCTGAGAGAGATCTACTGAGAGAGGAGATCTACCTGAAGTTAAGCT 312

QY 101 LysSerGlnGlnGlnGlySerLeuLysLeuGlnuAspLeuProThrValGlnuAlaProGly 120
Db 313 AAATCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTTACTGTTGAGGCTCTCGA 372
QY 121 AspProGlnGlnProGlnAsnAsnAlaHisArgAspGlyGlnuAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCAAGATTAATGCCCAAGGAGCAAAAGAGGAGATGACCAAGATCAT 432
QY 141 TTPArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGGCTATGAGAGGAGCCGCCCTGGGCCCGGGGTGTCCAGGCTGGCGGGCGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGAGTATTCGCCCCCAAGCTCGCCCTTCTGCCCCGCGCCCTCGCCCTTG 552
QY 181 GlnLeuLeuGlyPheGlnLeuLeuProProLeuProGlnuLeuArgLeuArgAsnGlyHis 200
Db 553 GAATCCTCGGCTTCGAGCTCCGCCCTCCAGAACCTGGGCTGGCGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnuMetAlaLeuGlyProGlyArgGlnTyr 220
Db 613 AGTGTGAACTGACCTGCTGCTGAGATGCTGTGGGTCCCGGGCGGAGATAC 672
QY 221 ArgAlaLeuGlnLeuHisIleuHisIleTyrGlyValAlaAlaArgProGlySerGlnHisThr 240
Db 673 CGGCTCTGACGCTGCACTTGCATCTGGGGGCTGCAAGTCTCCGGGCTCGGAGACACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnuIleHisValValHisIleuSerThrAlaPheAla 260
Db 733 GTGAAAGGCCACCGTTTCCCTGCGGAGATCCAGCTGGTTCACTCAGACAGCGCTTGGC 792
QY 261 ArgValAspGlnuAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln 280
Db 793 AGATTACACGAGGCTTGGGGCGCCCGGAGGCTGCGCGGTGGCGCGCTTCTTGAG 852
QY 281 GlnGlyProGlnGlnuAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnuIleAla 300
Db 853 GAGGAGCCGAGAGAAACAGTGTCTTATGAGCATGTGCTGTCTCCCTTGGAGAAATCGCT 912
QY 301 GlnGlnGlySerGlnuThrGlnuValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAGGCTCAGAGACTCAGGTCCAGAGCTGACATATCTGACATCTCCCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCAGCGCTACTTCCAAATATGAGGGGTCTGTGACTACCGCCCTGTGCCAGGGTGTG 1032
QY 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisIleThrLeuSer 360
Db 1033 ATCTGACGTGTGTTTAAACAGACAGTATGCTAGTGTCTAGAGCTCCACACCTCTCT 1092
QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGACCTGGGATCTCGGCTTACAGCTGAATCTCCGAGGAGACGACGCT 1152
QY 381 LeuAsnGlyArgValIleGlnuAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1153 TTGATGTGGGAGATTTGAGGCTCTCTGCTGAGGTGAGACACAGTCCCTCGGAGCT 1212
QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCAGTCACTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnuMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTGTGTGCACAGAGGTGCGCTTCTTGTGACATGAGAGAGACACAGAGA 1332
QY 441 ArgGlyThrIleGlyGlyValSerTyrArgProAlaGlnuValAlaGlnuThrGlyAla 459
Db 1333 AGGGAAACAAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCGGAGCTGAGGCC 1389

RESULT 8

ADK41803
ID ADK41803 standard; DNA, 1522 BP.
XX
XX AC ADK41803;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human MN gene sequence SegID1.
XX
XX KW carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
XX RV human; vertebrate; cytostatic; vaccine; gene therapy;
XX KW renal cell carcinoma; breast cancer; colorectal cancer; de; gene.
XX
XX OS Homo sapiens.
XX
XX FT Key Location/Qualifiers
XX FT CDS 13..1392
XX FT /*tag= a
XX FT /product= "Human MN protein"
XX
XX MN WO2004005348-A1.
XX
XX PD 15-JAN-2004.
XX
XX PF 22-FEB-2003; 2003WO-US005137.
XX
XX PR 23-MAY-2002; 2002US-0383068P.
XX PR 05-DEC-2002; 2002US-0431499P.
XX
XX PA (FARB) BAYER CORP.
XX PA (VIRO-) INST VIROLOGY.
XX
XX PL Zavada J, Pastorekova S, Pastorek J, Zavadova Z;
XX
XX DR WPI; 2004-083500/08.
XX DR P-PSDB; ADK41804.
XX
XX PT New soluble form of the carbonic anhydrase IX (CA IX) protein for
XX PT screening; diagnosing or prognosing diseases associated with abnormal
XX PT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
XX PT colorectal cancer.
XX
XX PS Disclosure; SEQ ID NO 1; 159pp; English.
XX
XX CC This invention relates to a novel soluble form of the carbonic anhydrase
XX CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
XX CC precancerous and/or cancerous cells of a vertebrate into a body fluid.
XX CC The invention may be useful for the development of compounds with a
XX CC cytosolic activity or a vaccine whilst the disclosed sequences may be
XX CC used for gene therapy. The protein whilst the disclosed sequences may be
XX CC diagnosing or prognosing diseases associated with abnormal expression of
XX CC carbonic anhydrase IX protein, such as precancerous and cancerous
XX CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.
XX CC The monoclonal antibody may also be used for treating or preventing
XX CC precancerous and cancerous diseases. The present sequence is that of the
XX CC gene which encodes the human MN protein of the invention.
XX
XX SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.:
Score: 1.62e-130 Length: 1522
Percent Similarity: 2424.00 Matches: 459
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-967-237A-2 (1-459) X ADK41803 (1-1522)

1 MetAlaProLeuGlyCysProSerProTyrPheuProLeuLeuIleProAlaProAlaProGly 20
13 ATGGCTCCCTGAGCCACGCCCTGGCTCCCTCTTTATCCCGGCCCTCTCAGGC 72

QY	21	LeuNHrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlyArgLeu	40
Db	73	CTCACTGGCAACTGCTGCTCACTGCTGCTTCTGATGCTGTCATCCCAAGAGTTG	132
QY	41	ProArgMetGlnGlyuAspSerProLeuGlyGlySerSerGlyGlyuAspAspProLeu	60
Db	133	CCCCGGATGACGAGAGGATTTCCCTCTGGGAGGAGGACTCTTCTGGGGAAGATGACCACTG	192
QY	61	GlyGlyGlnuAspLeuProSerGlyGlnuAspSerProArgGlyGlyuAspProGlyGly	80
Db	193	GCGCAGAGGAGATCTGCCCCAGTGAAGAGGATTTACCCACAGAGGAGGATTCACCCGGAAG	252
QY	81	GlyuAspLeuProGlyGlyGlyGlyuAspLeuProGlyGlyGlyuAspLeuProGlyValLysPro	100
Db	253	GAGGATCTACTGGAGAGGAGGAGATCTACTGGAGAGGAGGATCTTCACTGAAGTTAAAGCTT	312
QY	101	LysSerGlyGlyGlyGlySerLeuLysLeuGlyuAspLeuProThrValGlyuAlaProGly	120
Db	313	AAATCAGAAAGAGGGGCTCCCTCAAGTTAGAGATCTCACTAGTTGAGGGCTCTCGGA	372
QY	121	AspProGlnGlyuProGlnAspAsnAlaHisArgAspLysGlyGlyuAspAspGlnSerHis	140
Db	373	GATCTCTCAAGAACCCAGAAATMAATGCCACAGGACAAAGAAAGGAGATGACCAAGTAT	432
QY	141	ThrArgTyrGlyGlyAspProProThrProArgValSerProAlaCysAlaGlyArgPhe	160
Db	433	TGGGGCTATGAGAGCGACCCCGCTGGCGCCGGGGTGTCCTCCAGAGCTGGCGGGCGCTTC	492
QY	161	GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu	180
Db	493	CAGTCCCGAGGAGATCCGCCCCAGCTCGCCGCTTCTGCCCCGGCTTCGGCCCCCTTG	552
QY	181	GlyuLeuLeuGlyPheGlnLeuProProLeuProGlyuLeuArgLeuArgAsnGlyHis	200
Db	553	GAACTCCCTGGGCTTCCAGCTCCGGCGCTCCAGAACTCGCTGGCGCAATAGGCAC	612
QY	201	SerValGlnLeuThrLeuProProGlyLysGlnMetAlaLeuGlyProGlyArgGlyuThr	220
Db	613	AGTGTGCAACTGACCTTCGCTTCGGGGCTAGACATGGCTCTGGGGTCCGGCGGAGATAC	672
QY	221	ArgAlaLeuGlnLeuHisLysHisSThrGlyValAlaGlyArgProGlySerGlyuHisThr	240
Db	673	CGGGCTCTGACAGCTGCACTGCACTGGGGGGCTCAGAGTCGTCGGGGTGGGAGCACACT	732
QY	241	ValGlyGlyHisArgPheProAlaGlyuLysHisValValHisLysSerThrAlaPheAla	260
Db	733	GTTGAGAGGCCACCCCTTCCCTGCGCAGATCCACGTGGTTCACCTCAGACCGCCTTTGGC	792
QY	261	ArgValAspGlyuAlaLeuGlyArgProGlyGlyLeuAlaValLysuAlaAlaPheLeuGly	280
Db	793	AGAGTTGACAGAGGCTTGGGGCGCCCCGAGAGGCTTGGCCGTTGGCCCTTTCTGGAG	852
QY	281	GlyGlyProGlyGlyuAsnSerAlaTyrGlyGlyGlnLeuLeuSerArgLeuGlyuLysAla	300
Db	853	GAGGGCCCGGAAGAAACAGTGCCTATGACAGATTGCTGCTCCCTTGGAGAAATCGCT	912
QY	301	GlyGlyGlySerGlyuThrGlnValProGlyLysuAspLysSerAlaLeuLeuProSerAsp	320
Db	913	GAGGAGGCTCAGAGACTCAGGTCCTCCAGGACTGACATTTGCACTTCGCCCCCTTGAC	972
QY	321	PheSerArgTyrPheGlnTyrGlyGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	973	TTTCAAGCCGCTACTTCCATATAGAGGGGTCTCTGACTACACCGCCCTGTGGCCCAAGGTCTC	1032
QY	341	IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer	360
Db	1033	ATCTGCACTGTGTTTAAACAGACAGTGTGCTGAGTGTATGAGCGCTCCACACCTCTCT	1092
QY	361	AspThrLeuThrProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlyPro	380
Db	1093	GACACCTCTGGGAGACTGTGACTCTTCGGCTTACAGCTGAACCTTCCAGGACCGCAGCT	1152
QY	381	LeuAsnGlyArgValIleGlyuAlaSerPheProAlaGlyValAspSerSerProArgAla	400

Db 343 AATACAGAGAGAGGCTCCCTGAGTGAAGAGTACTACTGTTGAGGCTCTGGA 402
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 403 GATCTTCAGAGAACCCCGAATATATGCCACAGGAGCAAGAGGGAGATGACCAAGATCAT 462
Qy 141 TTPArGTYrGlyGlyAspProProTTPProTTPArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGGGCTATGAGAGCGACCGCCCTGGCCCGGGGTGTCCCAAGCTCTCGGGCGCGCTTC 522
Qy 161 GlnSerProValAspPheArgProGlnLeuAlaIaPheCysProAlaIaLeuArgProLeu 180
Db 523 CAGTCCCGGGTGAATATCCGCCCTGACCTGCGCTTGTCCCGGCGCTGCGCCCTG 582
Qy 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlyHis 200
Db 583 GAACTCTGGGCTTCCAGCTCCCGCCCTCCCAAACTGCGCCCTGGCCAAATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGluTyr 220
Db 643 AGTGTCAACTGACCTGCTCTCGGGCTAGAGATGCTGTGGGTCCCGGGCGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisIleuHisIleuGlyAlaIaIaGlyArgProGlySerGlnHisThr 240
Db 703 CGGGCTGTGACGCTGCACTGTGCACTGGGGGGCTGCAAGTGTCTCGGGCTCGAGCACACT 762
Qy 241 ValGlnGlyHisArgPheProAlaGluIleHisValAlaHisIleuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCGTTTCCCTGCGCGAGATCCAGCTGTTCACCTCAGCACCGCTTTGCC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTACAGAGGCTTGGGGCGCCCGGAGGCTGCGCGCTTGTGGCGCTTCTTGAG 882
Qy 281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGluIleAla 300
Db 883 GAGGGCCCGGAGAGAAACAGTCTATGAGAGATGTGCTGTCTTGGTGAAGAAATGCT 942
Qy 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGGCTCAGAGACTCAGGTCCAGAGCTGACATATCTGACATCCGCTTCTGAC 1002
Qy 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAGCCGTAATTCATATGAGGGGTCTCTGACTACCGCCCTGTGCCAGGGGTGC 1062
Qy 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaIysGlnLeuHisIleThrLeuSer 360
Db 1063 ATCTGACGTGTATTACACAGACAGTATGCTGATGCTTAAGACGCTCCACACCTCTCT 1122
Qy 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCTGTGGGGACCTGGGTGACTCTCGGCTACAGCTGAACCTTCGAGGAGGACACT 1182
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1183 TTGAATGGGGAGATGTGAGGCTCTCTCTCTGCTGAGGTGACACAGCTCTCGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaIaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCACTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
Qy 421 GlyLeuLeuPheAlaValIleThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCTCTTTTGTGTGCACAGCGTCCGCTTCTTGTGAGATGAGAGAGGACAGACAGA 1362
Qy 441 ArgGlyThrLysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGGAACAAAGGGGTGTGACTACCGCCACAGAGTACGAGACTGAGGCC 1419

RESULT 10
ABL62179
ID ABL62179 standard; DNA, 1552 BP.

XX ABL62179;
AC 15-MAY-2002 (first entry)
XX
XX
DE Colon adenocarcinoma related gene sequence SEQ ID NO: 516.
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN W0200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
XX 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236482P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.

XX PF 30-MAY-2001; 2001WO-US010838.

PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0231313P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 28-SEP-2000; 2000US-0236412P.
PR 29-SEP-2000; 2000US-0236891P.
PR 29-SEP-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237605P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.

XX (AVAL-) AVALON PHARM.
XX
PA Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;
XX MPI; 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 3753; 44pp; English.

CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABU7010), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous

CC	cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC	tumour
XX	Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
50	
Alignment Scores:	
Pred. No.:	1,65e-130
Score:	2424.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	Gaps: 0
US-09-967-237A-2 (1-459) x ABL65416 (1-1552)	
QY	1 MetAlaProLeuCySerProSerProTrpLeuProLeuLeuLeProAlaProAlaProGly 20
DB	43 ATGACCTCCCTGGGCCCAAGCCCTGGGCTCCCTGTTGATCCGGCCCCCTGCCAGGC 102
QY	21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
DB	103 CTCACCTGTGAACGTGCTGCTGTCACTGCTGCTTCGAGCCTGTCCATCCCAAGGTTG 163
QY	41 ProArgMetGlnGlnuAspSerProLeuGlyGlySerSerGlyuAspAspProLeu 60
DB	163 CCCCGATGAGAGGAGATTCCTCCCTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG 222
QY	61 GlyGlnGlnuAspLeuProSerGlnGlnuAspSerProArgGlnGlnuAspProProGlyGln 80
DB	223 GCGGAGAGGAGATTCGCCAGTAAAGAGATTCACCCAAGAGAGAGATCCACCCGAGAG 282
QY	81 GlnuAspLeuProGlyGlnGlnuAspLeuProGlyGlnGlnuAspLeuProGlnuValLysPro 100
DB	283 GAGGATCTACCTGAGAGAGAGAGATCTACCTGAGAGAGAGATCTAACCTGAAGTTAAAGCT 342
QY	101 LysSerGlnGlnGlnGlySerLeuLysLeuGlnuAspLeuProTrpValGlnuAlaProGly 120
DB	343 AAATTCAGAAAGAGAGGCTCCCTGAAGTTAGAGATTCACTACTGTTGAGGCTCTGGA 402
QY	121 AspProGlnGlnuProGlnuAsnAsnAlaHisArgAspLysGlnuLysAspAspGlnSerHis 140
DB	403 GATCTCAAGAAACCCAGAAATATGCCCAAGGAGCAAAAGAGGAGTGAACAGATCAT 462
QY	141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyValArgPhe 160
DB	463 TGGCGTTATGAGGCCACACCCGCCCTGGGCCCGGGGTGTCCAGAGCTCGCGGGCCGCTTC 522
QY	161 GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB	523 CAGTCCCCCGGTGGATTCGCCCCCAAGCTCGCGGCTTCTGCCCCGGCCCTCGGCCCTG 582
QY	181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnArgLysHis 200
DB	583 GAACCTCCTGGGCTTCAGAGCTCCGCGGCTCCAGAACTGCGCCGCAACAAAGGCCAC 642
QY	201 SerValGlnLeuThrLeuProProGlyLysGlnuMetAlaLeuGlyLysProGlyValArgGlnTyr 220
DB	643 AGGTGCACACTGACCTGCTCTCTGAGCTAGAGAGGCTCTGGGATCCCGGGCGGAGATAC 702
QY	221 ArgAlaLeuGlnLeuHisLysHisTrpGlyAlaAlaGlyArgProGlySerGlnuHisThr 240
DB	703 CGGGCTCTGAGGTGATGTGACAGTGGGGGTGTGAGTGTCTCGGGCTGGAGACACT 762
QY	241 ValGlnGlyHisArgPheProAlaGluLeuHisValValHisLysSerTrpAlaPheAla 260
DB	763 GTGGAAGGCCACCGTTTCCCTGCCAGATCCACGTTGTTCACTCCACACACCGCTTGGCC 822
QY	261 ArgValAspGlnuAlaLeuGlyValArgProGlyGlyLeuAlaValAlaAlaPheLeuGln 280
DB	823 AGAGTTGACGAGGCTTGGGGGCGCCCGGAGAGGCTTGCGCGTTCCTTCTGGAG 882
QY	281 GlnGlyProGlnGlnuAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnuAla 300

Db 883 GAGGCCCGGAGAAAACAGTCTATGACAGTTCCTGCTCGTGGAGAAATCGCT 942
Qy 301 GUGUGUGYserGluThrGlnValProGlyLeuAspIleSerValLeuLeuProSerAsp 320
Db 943 GAGGAGGCTCAGACCTCAGGTCCAGACATATGACATCTGCTGCTGAC 1002
Qy 321 PheSerArgIYrPheGlnIYrGluYserLeuThrThrProProCysAlaGlnIYrVal 340
Db 1003 TTCACCCCTACTTCCATATATAGAGGGGTCTGACTACACCCCTGTCGAGGGTTC 1062
Qy 341 ILeTPThrValPheAsnGlnThrValMetLeuSerAlaYseGlnLeuHISThrLeuSer 360
Db 1063 ATCTGAGCTGTGTTAACAGACAGTGAATGCTGAGGTCTAACAGACTCCACACCTCTCT 1122
Qy 361 AspThrLeuTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCCGTGGGAGCTGTGTACTCTCGCTACAGCTGAATCTCCAGACGAGAGCT 1182
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1183 TTGAATGGCGAGTATAGAGCTCTTCTCTGCTGAGTGAAGACAGTCTCGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCCAGTCCAGCTGAATCTGCTGCTGCTGCTGAGTGAATCTGCTGCTGCTGCT 1302
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnIleArg 440
Db 1303 GGCCTCTTTTGTGCTGTCACGCGTCCGCTTCTTGTGACATAGAAAGCAGACAGA 1362
Qy 441 ArgGlyThrIYrGlyGlyValSerIYrArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGAGACCAAGGGGGTGTGAGTACCCGCCAGACAGGTAGCCGAGACTGAGACC 1419

RESULT 12

ABL68346
ID ABL68346 standard; DNA; 1552 BP.

XX ABL68346;

XX AC 15-MAY-2002 (first entry)

XX DT 15-MAY-2002 (first entry)

XX DE Kidney cancer related gene sequence SEQ ID NO: 6683.

XX XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
gene; ds.

XX XX Homo sapiens.

XX OS WO200194629-A2.

XX PN 13-DEC-2001.

XX PF 30-MAY-2001; 2001WO-US010838.

XX XX 05-JUN-2000; 2000US-0209473P.

XX PR 05-JUN-2000; 2000US-0209531P.

XX PR 18-SEP-2000; 2000US-0231133P.

XX PR 18-SEP-2000; 2000US-0231617P.

XX PR 20-SEP-2000; 2000US-0234009P.

XX PR 20-SEP-2000; 2000US-0234034P.

XX PR 20-SEP-2000; 2000US-0234052P.

XX PR 22-SEP-2000; 2000US-0234509P.

XX PR 22-SEP-2000; 2000US-0234567P.

XX PR 25-SEP-2000; 2000US-0234923P.

XX PR 25-SEP-2000; 2000US-0235077P.

XX PR 25-SEP-2000; 2000US-0235083P.

XX PR 25-SEP-2000; 2000US-0235134P.

XX PR 25-SEP-2000; 2000US-0235280P.

XX PR 26-SEP-2000; 2000US-0235637P.

PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 02-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAIL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;
XX MPI: 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 6683; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
CC tumour

XX SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,656-130	Length:	1552
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-967-237A-2 (1-459) x ABL68346 (1-1552)

Qy 1 MetAlaProLeuGlyProSerProTyrLeuProLeuIleProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGCTCCAGCCCTGCTCTGTTGATCCGCGGCTCTGCTCAGGC 102

QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
 DB 103 CTCACCTGCAACGCTGCTCTCACTGCTGTTGATGCTGCATCCCAAGAGTTG 162
 QY 41 ProArgMetGlnuAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
 DB 163 CCCCAGATGAGAGGAGATTCCCCCTTGAGAGAGCTTCTGGAGGAATGACCCACTG 222
 QY 61 G1yGluGluAspLeuProSerGluGluAspSerProArgGluuAspProProGlyGlu 80
 DB 223 GCGGAGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGATCCACCCGAGAG 282
 QY 81 GluAspLeuProGlyGluuAspLeuProGlyGlyGluuAspLeuProGlyuValysPro 100
 DB 283 GAGGATCTACCTGGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAGTTAACT 342
 QY 101 LysSerGluGluGlySerLeuLeuLeuGluAspLeuProThrValGluuAProGly 120
 DB 343 AAATCAGAAAGAGAGGCTCCCTGAAGTATGAGATCTACTCTGTTGAGGCTCTGGA 402
 QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGluAspAspGlnSerHis 140
 DB 403 GATCTCAAGAACCCCAATATATGCCCAAGGACAAAGAGAGATGACACAGATCAT 462
 QY 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
 DB 463 TGGGCTATGAGAGCGACCCGCCCTGGCCCGGGGTGCCAGCTCGCGGGCGCTTC 522
 QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
 DB 523 CAGTCCCGGTGATATCCGCCCACTCGCCCTTCTGCGCGGCCCTGCGGCCCTCG 582
 QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlyuLeuArgLeuArgAsnAsnGlyHis 200
 DB 583 GAATCTTGAGGCTTCCAGCTCCGCCCTCCAGAACTGGCGCTGCCCAATAGGCAC 642
 QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
 DB 643 AGTGTGCACTGACCTGCTGCTGGGCTAGAGATGCTCTGGGTCCCGGGCGGAGTAC 702
 QY 221 ArgAlaLeuGlnLeuHisIleuHisIleuProGlyValAlaIleuArgProGlySerGlnHisIleu 240
 DB 703 CGGGCTGTGAGCTGCACTGTGCACTGGAGGCTGCACTGCTGGAGCAACT 762
 QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisIleuSerThrAlaPheAla 260
 DB 763 GTGGAAGGCCACCTTCCCTGCCGAGATCCAGCTGCTCACCCTCACACCGCTTGGC 822
 QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
 DB 823 AGAGTTACAGAGGCTTGAGGCGCGCGGAGGCTGCGCTGTGGCGCTTCTGGAG 882
 QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
 DB 883 GAGGCGCCGAGAAACAGTGTCTATGAGAGATGTGCTGCTGCTGGAGAAATGCT 942
 QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
 DB 943 GAGGAAGGCTCAGAGATCCAGGCTCCAGACTGACATATCTGACCTCCCTCTGAC 1002
 QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
 DB 1003 TTGAGCGGCTACTTCAATATGAGGGGTCTCTGACTACACCGCCCTTGCCAGGGTGC 1062
 QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisIleuLeuSer 360
 DB 1063 ATCTGAGCTGTGTTAACTGAGACAGATGCTGAGCTTAAGCAGCTCCACACCTCTCT 1122
 QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
 DB 1123 GACACCTGTGGGAGCTGTGATCTCGGCTACAGCTGAATCTCCAGAGCAGCAGCT 1182

QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
 DB 1183 TTGAATGGCGAGATGATGAGGCTCTTCTGCTGAGACTGACAGACATCTCGGGCT 1242
 QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
 DB 1243 GCTGAGCACTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
 QY 421 G1yLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
 DB 1303 GGCCTCTTTTCTGTGACACGCTGCTGCTCTTGTGTGAGATGAGAGCAGCAGAGA 1362
 QY 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 460
 DB 1363 AGGGAAACCAAGGGGTGTGAGCTACCGCCAGAGAGGTAGCCGAGCTGAGCC 1419
 RESULT 13
 ABX76385
 ID ABX76385 standard; DNA; 1552 BP.
 XX
 AC ABX76385;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polynucleotide #249.
 XX
 KW Lung cancer-associated polynucleotide; gene; ds; cytosolic; emphysema;
 KW anti-inflammatory; antispasmodic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX
 OS Unidentified.
 XX
 PN WO20028643-A2.
 PD 31-OCT-2002.
 XX
 PF 18-APR-2002; 2002WO-US012476.
 XX
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 03-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (BOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Aziz N, Murray R;
 XX
 DR WPI; 2003-093161/08.
 DR P-PSDB; ABUS6656.
 XX
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX
 PS Claim 22; Page 379-380; 453bp; English.
 XX
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,

XX WPI: 2003-093161/08.
DR P-PSDB; ABUS6408.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 189; 453bp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1 656-130 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-967-237a-2 (1-459) x ABX76124 (1-1552)
QY 1 MetAlaProLeuCyProSerProTrpLeuProLeuLeuProAlaProAlaProGly 20
DB 43 ATGGCTCCCTGTCAGCCAGCCCTGGCTCCTCTGTGATCCGGCCCTGTCAGGC 102
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 103 CTCACGTGTGCAACTGCTGTCTGCTCTGCTGATGCTGCTGCAATCCCAAGGTTG 162
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB 163 CCCCAGATGCAAGAGATTCCCTTGGAGAGAGGCTCTTGGAGAGATGACCCACTG 222
QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProGlyGlu 80
DB 223 GCGCAGAGAGATGCGCCAGTGAAGAGATTCAACCGAGAGAGATCCACCGGAGAG 282
QY 81 GlnAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyValLeuPro 100
DB 283 GAGATCTTACCTGAGAGAGAGATCTAATCGAGAGAGATCACTGAAGTTAAACCT 342
QY 101 LysSerGlnGluGlnGlySerLeuLeuGlnGluAspLeuProThrValGlnAlaProGly 120
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QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspArgGlnGlyAspAspGlnSerHis 140
DB 403 GATCCTCAAGAACCCGAGATTAATGCCACAGGGAAGAGAGGAGTGAACAGATCAT 462
QY 141 TTPArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160

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DB 763 GTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTCACCTCAGACCCGCTTGGCC 822
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DT 11-MAR-2004 (first entry)
XX
DE Cancer detection method related gene #6.
XX
KW de; cancer; gene expression;

Db 1363 AGGGGAACCAAGGGGGTGTGACCTACCGCCAGAGAGGTAGCCGAGACTGTGAGCC 1419

Search completed: August 19, 2005, 22:26:00
Job time : 785 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 21:34:10 ; Search time 248 Seconds

(without alignments)
3028.432 Million cell updates/sec

Title: US-09-967-237A-2

Perfect score: 2424

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-DEV_TIMEOUT=130-WARN_TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2424	100.0	1522	2	US-08-477-504A-1	Sequence 1, Appl
3	2424	100.0	1522	2	US-08-486-756A-1	Sequence 1, Appl
4	2424	100.0	1522	2	US-08-485-862B-1	Sequence 1, Appl
5	2424	100.0	1522	3	US-08-787-739-1	Sequence 1, Appl
6	2424	100.0	1522	3	US-08-487-077A-1	Sequence 1, Appl
7	2424	100.0	1522	3	US-08-485-863A-1	Sequence 1, Appl
8	2424	100.0	1522	3	US-08-485-049D-1	Sequence 1, Appl
9	2424	100.0	1522	3	US-09-178-115-1	Sequence 1, Appl
10	2424	100.0	1522	3	US-09-177-776-1	Sequence 1, Appl
11	2424	100.0	1522	4	US-09-772-719B-1	Sequence 1, Appl
12	2424	100.0	1522	4	US-08-260-150-5	Sequence 5, Appl

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14	2420	99.8	1552	4	US-09-949-016-4332		Sequence 4332, Ap
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18	2036	84.0	1397	1	US-07-964-589-1		Sequence 1, Appli
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20	1253.5	51.7	11237	4	US-09-949-016-11913		Sequence 11913, A
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24	1176.5	48.5	10898	2	US-08-486-756A-5		Sequence 5, Appli
25	1176.5	48.5	10898	2	US-08-485-862B-5		Sequence 5, Appli
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27	1176.5	48.5	10898	3	US-08-487-077A-5		Sequence 5, Appli
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38	714	29.5	415	3	US-08-485-863A-28		Sequence 28, Appli
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ALIGNMENTS

RESULT 1

US-08-481-658B-1
; Sequence 1, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-435-2034

TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs

LENGTH: 1322 base pairs
TYPE: nucleic acid

STANDARDS: 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 1.10, 1.11, 1.12, 1.13, 1.14, 1.15, 1.16, 1.17, 1.18, 1.19, 1.20, 1.21, 1.22, 1.23, 1.24, 1.25, 1.26, 1.27, 1.28, 1.29, 1.30, 1.31, 1.32, 1.33, 1.34, 1.35, 1.36, 1.37, 1.38, 1.39, 1.40, 1.41, 1.42, 1.43, 1.44, 1.45, 1.46, 1.47, 1.48, 1.49, 1.50, 1.51, 1.52, 1.53, 1.54, 1.55, 1.56, 1.57, 1.58, 1.59, 1.60, 1.61, 1.62, 1.63, 1.64, 1.65, 1.66, 1.67, 1.68, 1.69, 1.70, 1.71, 1.72, 1.73, 1.74, 1.75, 1.76, 1.77, 1.78, 1.79, 1.80, 1.81, 1.82, 1.83, 1.84, 1.85, 1.86, 1.87, 1.88, 1.89, 1.90, 1.91, 1.92, 1.93, 1.94, 1.95, 1.96, 1.97, 1.98, 1.99, 2.00, 2.01, 2.02, 2.03, 2.04, 2.05, 2.06, 2.07, 2.08, 2.09, 2.10, 2.11, 2.12, 2.13, 2.14, 2.15, 2.16, 2.17, 2.18, 2.19, 2.20, 2.21, 2.22, 2.23, 2.24, 2.25, 2.26, 2.27, 2.28, 2.29, 2.30, 2.31, 2.32, 2.33, 2.34, 2.35, 2.36, 2.37, 2.38, 2.39, 2.40, 2.41, 2.42, 2.43, 2.44, 2.45, 2.46, 2.47, 2.48, 2.49, 2.50, 2.51, 2.52, 2.53, 2.54, 2.55, 2.56, 2.57, 2.58, 2.59, 2.60, 2.61, 2.62, 2.63, 2.64, 2.65, 2.66, 2.67, 2.68, 2.69, 2.70, 2.71, 2.72, 2.73, 2.74, 2.75, 2.76, 2.77, 2.78, 2.79, 2.80, 2.81, 2.82, 2.83, 2.84, 2.85, 2.86, 2.87, 2.88, 2.89, 2.90, 2.91, 2.92, 2.93, 2.94, 2.95, 2.96, 2.97, 2.98, 2.99, 3.00, 3.01, 3.02, 3.03, 3.04, 3.05, 3.06, 3.07, 3.08, 3.09, 3.10, 3.11, 3.12, 3.13, 3.14, 3.15, 3.16, 3.17, 3.18, 3.19, 3.20, 3.21, 3.22, 3.23, 3.24, 3.25, 3.26, 3.27, 3.28, 3.29, 3.30, 3.31, 3.32, 3.33, 3.34, 3.35, 3.36, 3.37, 3.38, 3.39, 3.40, 3.41, 3.42, 3.43, 3.44, 3.45, 3.46, 3.47, 3.48, 3.49, 3.50, 3.51, 3.52, 3.53, 3.54, 3.55, 3.56, 3.57, 3.58, 3.59, 3.60, 3.61, 3.62, 3.63, 3.64, 3.65, 3.66, 3.67, 3.68, 3.69, 3.70, 3.71, 3.72, 3.73, 3.74, 3.75, 3.76, 3.77, 3.78, 3.79, 3.80, 3.81, 3.82, 3.83, 3.84, 3.85, 3.86, 3.87, 3.88, 3.89, 3.90, 3.91, 3.92, 3.93, 3.94, 3.95, 3.96, 3.97, 3.98, 3.99, 4.00, 4.01, 4.02, 4.03, 4.04, 4.05, 4.06, 4.07, 4.08, 4.09, 4.10, 4.11, 4.12, 4.13, 4.14, 4.15, 4.16, 4.17, 4.18, 4.19, 4.20, 4.21, 4.22, 4.23, 4.24, 4.25, 4.26, 4.27, 4.28, 4.29, 4.30, 4.31, 4.32, 4.33, 4.34, 4.35, 4.36, 4.37, 4.38, 4.39, 4.40, 4.41, 4.42, 4.43, 4.44, 4.45, 4.46, 4.47, 4.48, 4.49, 4.50, 4.51, 4.52, 4.53, 4.54, 4.55, 4.56, 4.57, 4.58, 4.59, 4.60, 4.61, 4.62, 4.63, 4.64, 4.65, 4.66, 4.67, 4.68, 4.69, 4.70, 4.71, 4.72, 4.73, 4.74, 4.75, 4.76, 4.77, 4.78, 4.79, 4.80, 4.81, 4.82, 4.83, 4.84, 4.85, 4.86, 4.87, 4.88, 4.89, 4.90, 4.91, 4.92, 4.93, 4.94, 4.95, 4.96, 4.97, 4.98, 4.99, 5.00, 5.01, 5.02, 5.03, 5.04, 5.05, 5.06, 5.07, 5.08, 5.09, 5.10, 5.11, 5.12, 5.13, 5.14, 5.15, 5.16, 5.17, 5.18, 5.19, 5.20, 5.21, 5.22, 5.23, 5.24, 5.25, 5.26, 5.27, 5.28, 5.29, 5.30, 5.31, 5.32, 5.33, 5.34, 5.35, 5.36, 5.37, 5.38, 5.39, 5.40, 5.41, 5.42, 5.43, 5.44, 5.45, 5.46, 5.47, 5.48, 5.49, 5.50, 5.51, 5.52, 5.53, 5.54, 5.55, 5.56, 5.57, 5.58, 5.59, 5.60, 5.61, 5.62, 5.63, 5.64, 5.65, 5.66, 5.67, 5.68, 5.69, 5.70, 5.71, 5.72, 5.73, 5.74, 5.75, 5.76, 5.77, 5.78, 5.79, 5.80, 5.81, 5.82, 5.83, 5.84, 5.85, 5.86, 5.87, 5.88, 5.89, 5.90, 5.91, 5.92, 5.93, 5.94, 5.95, 5.96, 5.97, 5.98, 5.99, 6.00, 6.01, 6.02, 6.03, 6.04, 6.05, 6.06, 6.07, 6.08, 6.09, 6.10, 6.11, 6.12, 6.13, 6.14, 6.15, 6.16, 6.17, 6.18, 6.19, 6.20, 6.21, 6.22, 6.23, 6.24, 6.25, 6.26, 6.27, 6.28, 6.29, 6.30, 6.31, 6.32, 6.33, 6.34, 6.35, 6.36, 6.37, 6.38, 6.39, 6.40, 6.41, 6.42, 6.43, 6.44, 6.45, 6.46, 6.47, 6.48, 6.49, 6.50, 6.51, 6.52, 6.53, 6.54, 6.55, 6.56, 6.57, 6.58, 6.59, 6.60, 6.61, 6.62, 6.63, 6.64, 6.65, 6.66, 6.67, 6.68, 6.69, 6.70, 6.71, 6.72, 6.73, 6.74, 6.75, 6.76, 6.77, 6.78, 6.79, 6.80, 6.81, 6.82, 6.83, 6.84, 6.85, 6.86, 6.87, 6.88, 6.89, 6.90, 6.91, 6.92, 6.93, 6.94, 6.95, 6.96, 6.97, 6.98, 6.99, 7.00, 7.01, 7.02, 7.03, 7.04, 7.05, 7.06, 7.07, 7.08, 7.09, 7.10, 7.11, 7.12, 7.13, 7.14, 7.15, 7.16, 7.17, 7.18, 7.19, 7.20, 7.21, 7.22, 7.23, 7.24, 7.25, 7.26, 7.27, 7.28, 7.29, 7.30, 7.31, 7.32, 7.33, 7.34, 7.35, 7.36, 7.37, 7.38, 7.39, 7.40, 7.41, 7.42, 7.43, 7.44, 7.45, 7.46, 7.47, 7.48, 7.49, 7.50, 7.51, 7.52, 7.53, 7.54, 7.55, 7.56, 7.57, 7.58, 7.59, 7.60, 7.61, 7.62, 7.63, 7.64, 7.65, 7.66, 7.67, 7.68, 7.69, 7.70, 7.71, 7.72, 7.73, 7.74, 7.75, 7.76, 7.77, 7.78, 7.79, 7.80, 7.81, 7.82, 7.83,

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

8-477-504A-1

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Pred. No.:	7.09e-202	Length:	1522
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Score:	2424.00	Matches:	459
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Percent Similarity:	100.00%	Conservative:	0
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Best Local Similarity:	100.00%	Mismatches:	0
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Query Match:	100.00%	Indels:	0
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DB:	2	GAPs:	0
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Db	853	GAGGGCCCCGAGAAACAGTGCGCTATGAGCAGTTGGCTGTCCGTTGGAGAAATCCCT	912
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; Patent No. 5981711			
; GENERAL INFORMATION:			
; APPLICANT: Zavada, Jan			
; APPLICANT: Pastorekova, Silvia			
; APPLICANT: Pastorek, Jaromir			
; TITLE OF INVENTION: MN Gene and Protein			
; NUMBER OF SEQUENCES: 86			
; CORRESPONDENCE ADDRESSES:			
; ADDRESSEE: Leona L. Lauder			
; STREET: 6 Mariposa Court			
; CITY: Tiburon			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94920			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.30 (ERO)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/486,756A			
; FILING DATE: 07-JUN-1995			
; CLASSIFICATION: 424			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/260,190			
; FILING DATE: 15-JUN-1994			
; ATTORNEY/AGENT INFORMATION:			

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.JC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-756A-1

Alignment Scores:
Pred. No.: 7,09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-967-237A-2 (1-459) x US-08-486-756A-1 (1-1522)

QY 1 MetAlaProLeuCySProSerProTPrLeuProLeuLeuIeProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTCGCTCCCGAGGCTGGCTCTGTTGATCCCGAGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACCTGGCAACTGCTGCTGTCACTGCTGCTTGTGATGCTTCCATCCCAAGGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCGATGCGAGGAGATTCCCTTGGAGAGGCTTCTTGGGAAAGATGACCCACTG 192
QY 61 GLyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 193 GGGCAGAGGATCTGCCAGTGAAGAGATTCACTCCAGAGAGAGATCCACCGGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValIlePro 100
Db 253 GAGGATCTACCTGGAGAGAGGATCTACCTGAGAGGAGATCTACCTGAAGTTAAGCT 312
QY 101 LysSerGluGluGlySerLeuLeuGluGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGGGCTCCCTTAAGTTAGAGATCTACTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGluAspAspGlnSerHis 140
Db 373 GATCTCAAGAACCCCGAATATATGCCACAGGACAAAGAGGATGACCAAGTCAT 432
QY 141 TrpArgTyrGlyAspProProTPrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCATGGAGCGACCGCGCTGGCGCCCGGGGTGCCACGCTGGCGGCGGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCACCTGCGCTTTCGCGCGGCGCTGCGCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuAspProGluLeuArgLeuArgAsnAsnGlyHis 200
Db 553 GAATCTCTGGGCTTCCAGCTCCCGCTCCCAAACTGCGCTGCGGCAAAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTGAACATGACCTGCTCTGGGCTAGAGATGGCTGGGCTCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaAlaGlyArgProGlySerGlnHisThr 240

Db 673 CGGGCTTCGAGCTGCATCTGCATCGGGGGGCTGCAGGCTCTCCGGGCTCGAGCACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAAGCCACCGTTTCCCTGCGAGATCCAGTGTTCACCTTCAGACACGGCTTTGCC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGATTGACGAGGCTTTGGGGCCCGGGAGGCTGGCCGTGTGGCCGCTTCTGGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerTrpLeuGluGluIleAla 300
Db 853 GAGGCGCGGAAAGAAACAGTGTCTATGACAGATGCTGTCTGTGGAAAGAAATGCT 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGCTCAGAGACTCAGTCCAGAGCTGGAACATATCTGCATCTCCGCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340
Db 973 TTCAGCCGTAATTCCAAATATGAGGGGTCTGTACTAACACCGCTGTGCCAGGGTGTG 1032
QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaIleGlnLeuHisThrLeuSer 360
Db 1033 ATCTGACGTGTGTTAACCAAGACAGTATGCTGATGCTAAGACGCTCCACACCTCTCT 1092
QY 361 AspThrLeuThrProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGCCTGGTGACTCTCGGCTACAGCTGAACCTTCGAGGAGAGGACCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProAlaGlyAla 400
Db 1153 TTGAATGGCGAGATGATTTGAGGCTCTCTCCGCTGAGTGAAGACATCTCCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGGCTGGTGAATCTTAAGCCCTGGTTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTCTGTCACACAGCTCGGCTCTGTGTGCAATGAGAAAGCACAGAGA 1332
QY 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAAACCAAGGGGTGTGAGCTACCGCCACAGAGGTACCGAGACTGAGGCC 1389

RESULT 4
US-08-485-862B-1
Sequence 1, Application US/08485862B
Patent No. 5989838
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MY Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-787-739-1

Alignment Scores:
Pred. No.: 7,09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-967-237A-2 (1-459) x US-08-787-739-1 (1-1522)

QY 1 MetAlaProLeuCyProSerProTriPLeuProLeuLeuIleProAlaProAlaProGly 20
DB 13 ATGGCTCCCTGTCGCCAGCCCTGGCTCCCTGTTGATCCCGCCCTGCTCCAGGC 72

QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 73 CTCACCTGGAACGCTGCTGTCTGCTGCTTGTGATGCTGTCATCCCAAGGTTG 132

QY 41 ProArgMetGlnLeuAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB 133 CCCCGAGTGCAGGAGATTCCCCCTGGAGGAGGCTTCTGGGGAAGTGAACCACTG 192

QY 61 G1GluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
DB 193 GGCAGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGGATCCACCCGGAGAG 252

QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
DB 253 GAGGATCTACCTGAGAGAGGAGATCTACCTGAGAGAGGATCTACCTGAAGTTAAGCT 312

QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120

DB 313 AAATCAGAAAGAGGGCTCCGAAATTAGAGAACTTACCTGCTGGGCTCCGGA 372

QY 121 AspProGlnGluProGlnAlaAlaHisArgAspLysGluGlyAspArgLysSerHis 140

DB 373 GATCTCAAGAACCCCAAGTAATGCCCAAGGACCAAGAGGAGATGCCAAGTCAAT 432

QY 141 TrpArgTyrGlyGlyAspProProTriProArgValSerProAlaCysAlaGlyArgPhe 160

DB 433 TGGGCTATAGAGGCGACCCGCCCTGGCCCGGGGTGTCCTCCAGCTCGCGGGCCGCTTC 492

QY 161 GlnSerProValAspLysArgProGlnLeuAlaAlaPheYsProAlaLeuArgProLeu 180

DB 493 CAGTCCCGGTGATATCCGCCCCCAGCTCGGCTTGCCCGGCGCTCCGCCCCCTG 552

QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAlaHis 200

DB 553 GAACTCTGGGCTTCCAGCTCCGCGCTCCCAAGAACTGGGCTGGCAATGGCCAC 612

QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220

DB 613 AGTGTCAATGACCTGCTCTGGGCTAGAGATGGCTCTGGGCTCCGGGCGGAGTAC 672

QY 221 ArgAlaLeuGlnLeuHisLeuHisSerProGlyAlaAlaGlyArgProGlySerGlnHisThr 240

DB 673 CGGCTCTGAGCTGATGCACTGCACTGGGGGCTGCAAGTCTCGGAGTGGACACT 732

QY 241 ValGluGlyHisArgPheProAlaGluLeuHisValAlaHisLeuSerThrAlaPheAla 260

DB 733 GTGGAAAGCCACCGTTCCCTGCGAGATCCAGTGTTCACCTCAAGCACCGGCTTTGCC 792

QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280

DB 793 AGAGTTGACAGAGCTTGGGGCGCCCGGGAGGCTGGCCGTGTGGCCGCTTTCGGAG 852

QY 281 GluGlyProGluGluLysSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluLeuAla 300

DB 853 GAGGGCCCGAAGAAACAGTGCCTATGAGCAATGCTGTCTGCTTGAAGAAATCGCT 912

QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320

DB 913 GAGGAAGCTCAAGACTCAAGTCCAGAGCTGCAATATCTGCACTCCGCTCTGAC 972

QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340

DB 973 TTCAGCCGCTAATCCAAATATGAGGGGTCTGTGACTACACCGCCCTGCGCGGTGTC 1032

QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360

DB 1033 ATCTGACTGTGTTTAAACAGACAGTATGCTGATGCAAGCTCCACACCTCTCT 1092

QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380

DB 1093 GACACCTTGAGGAGACTGTGACTCTCGGCTACACTGAATCTCCGAGGAGCAGGCT 1152

QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400

DB 1153 TTGAATGGCGAGATGATTGAGGCTCTCTCCCTGCTGAGTGAAGCAGTCTCCGGGCT 1212

QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLysLeuAlaLeuValPhe 420

DB 1213 GCTGAGCAATTCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272

QY 421 G1LeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440

DB 1273 GGCCTCTTTTCTGTGACACGCTGCGCTTCTGTGCAAGTATGAAGGACGACACAG 1332

QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459

DB 1333 AGGGAAACCAAGGGGTGTGAGTACCGCCGACAGAGGTAGCCGAGACTGGAGCC 1389

RESULT 6
US-08-487-077A-1

RESULT 7
US-08-485-863A-1
Sequence 1, Application US/08485863A
Patent No. 6093548
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: NM Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,863A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-485-863A-1
Alignment Scores:
Pred. No.: 7.09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 3
US-09-967-237A-2 (1-459) x US-08-485-863A-1 (1-1522)
QY 1 MetaAlaProLeuCySPSeProTPrLeuProLeuLeuIleProAlaProAlaProGly 20
DB 13 ATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTGATCCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 73 CTCACCTGTGCACTGCTGTCTGCTCTGCTGTGATGCTGTCATCCATCCCAAGAGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerGlyGlyAspAspProLeu 60
DB 133 CCCCAGATGAGAGGAGGATTCCTCCCTTGAGAGAGGCTCTTGGGGAAGATGACCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
DB 193 GGGAGAGAGATCTGCCCACTGAAGAGATTCCACCCAGAGAGAGATCCACCCGAGAG 252

QY 81 GluAspLeuProGlyGlyGluAspLeuProGlyGlyGluAspLeuProGlyValIysPro 100
DB 253 GAGGATCTACCTGAGAGAGAGATCTTACCTGAGAGAGAGATCTTACCTGAAGTTAAGCCT 312
QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
DB 313 AAATCAGAAAGAGAGGCTCCCTGAAGATTAGAGAGATCTTACTCTTTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
DB 373 GATCTTCAGAACCCCAAGATTATGCTCCACAGGAGCAAAAGAGGAGATGACCAAGATCAT 432
QY 141 TTPArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
DB 433 TGGCGCTATGAGAGGCAAGCCCGCTGAGGCTCCCAAGCTGCGGAGGCTCCCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 493 CAGTCCCGGTGATATCCGCCCAAGCTCGCCGCTTGTGCCCGCCCTGCGCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgPheAsnAsnGlyHis 200
DB 553 GAACCTCGGGCTTCCAGCTCCGCGCTCCCAAGACTGCGCTGCGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
DB 613 AGTGCAACTGACCTGCTCTGCGGCTAAGATGCTGCGGCTCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisSerProGlyAlaAlaGlyArgProGlySerGlyHis 240
DB 673 CGGGCTCTGAGCTGATGTCATGCACTGGGGGCTGCAAGTCTGGGCTCGGAGCACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
DB 733 GTGGAAGGCCACCGTTTCTCTGCGAGATCCACGTGTTTCACTTCAGCACCGCCTTGGC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280
DB 793 AGAGTTGACAGAGCTTGGGGCGCCCGGAGGCTGGCGTGTGGCCGCTTTCGGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
DB 853 GAGGGCCCGGAATAAACAAGTGTCTATGAGCAATTCTGTCTGTGGAAGAAATCGCT 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
DB 913 GAGGAAGCTCAGAGACTCAGGCTCCAGAGCTGAGCATATCTGCACTCTCGCCCTGAGC 972
QY 321 PheSerArgTyrPheGlnTyrGlyGlySerLeuThrProProCysAlaGlnGlyVal 340
DB 973 TTCAGCCGCTACTTCCAAATATGAGGGGTCTGTACATACACCGCCCTGTGCGGGTGTG 1032
QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisSerHisLeuSer 360
DB 1033 ATCTGACGTGTGTTAACCAAGACATGATGCTGATGAGTCTTCAACACCTCTCT 1092
QY 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
DB 1093 GACACCTGTGGGAGACTGGTACTCTCGGCTACACCTGAACCTTCCAGAGAGAGAGCCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProAlaAla 400
DB 1153 TTGAATGGGAGATGATTAGAGGCTCTCCCTCGCTGAGTGAAGCAGCATCTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
DB 1213 GCTGACCACTCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
DB 1273 GGCCTCTTTTCTGTCTACACAGCTTCGCGCTTCTGTGTCAATGAGAGGAGCAGCAGA 1332

QY 441 ArgGlyThrIyGlyValSerTyrArgProAlaGluValAlaGluThrGlyVala 459
DB 1333 AGGGAGACCAAGGGGGTGTGAGCTACCGCCAGAGAGGTAGCCGAGACTGAGGCC 1389

RESULT 8
US-08-485-049D-1
Sequence 1, Application US/08485049D
Patent No. 6204370

GENERAL INFORMATION:

APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-485-049D-1

Alignment Scores:

Pred. No.: 7.09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-967-237a-2 (1-459) x US-08-485-049D-1 (1-1522)

QY 1 MetAlaProLeuCyProSerProTrpLeuProLeuLeuLeuProAlaProAlaProGly 20
DB 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTGTGTGATCCCGACCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 73 CTCACCTGGCAACTGCTGTCTGTCACGTGCTTCTGATGCTGCTCATCCCAAGAGTTG 132
QY 41 ProArgMetGlnGlnAspSerProLeuGlyGlyGlySerSerGlyGlnAspAspProLeu 60
DB 133 CCCCAGATGCAAGAGATTCCCTCTTGGAGAGAGGCTCTTCTGGGGAGAGATGACCACTG 192

QY 61 GlyGluGluAspLeuProSerGlyGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGGAGAGAGATCTGCCAGTGAAGAGATTCAACCAAGAGAGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGlyGluGluAspLeuProGlyGlyGluGluAspLeuProGlyVal 100
DB 253 GAGGATCTACCTGGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAGTTAAGCT 312
QY 101 LysSerGluGluGlyGlySerLeuLeuLeuLeuLeuLeuProThrValGlnAlaProGly 120
DB 313 AAATCAGAGAGAGAGAGGCTCTGAAGTTAAGAGATCTACCTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgArgAspGlyGlyGlyAspAspGlnSerHis 140
DB 373 GATCTCTCAAGAACCCCAATATATATCCCAAGGACAAAGAGAGAGATGACCAAGTCAAT 432
QY 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
DB 433 TGGCGCTATGAGAGGACCCGCCCTGGCCCGGGGTGCCAGCCTGGCGGGCGGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 493 CAGTCCCGGTGATATCCGCCGCCAGCTCCCGCTTCTGCCCCGCCCTCGCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
DB 553 GAACTCTGGGCTTCCAGCTCCGCCCTCCCAAGACTCCGCTCGGACAAATGAGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
DB 613 AGTGCAACTGACCTCTCTGAGCTAAGATGAGTCTGGGTCGGGCGGGAGATAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyValAlaAlaGlyArgProGlySerGlnHisThr 240
DB 673 CGGGCTCTGACGTGCATCTGCATCTGAGGGGCTGAGGTCGTCCGGCTCGAGACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValIleHisLeuSerThrAlaPheAla 260
DB 733 GTGAGAGCCACCGTTTCCCTCCGAGATCCACGTGTCTCACTAGACACCGCTTTC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
DB 793 AGAGTTGACGAGGCTTGAGGCGCCCGGAGGCTCGCGTGTGGCCGCTTCTGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAla 300
DB 853 GAGGCGCCGAGAGAAACAGAGCTTATGACAGATGCTGCTGCTTGGAAAGAAATTCCT 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
DB 913 GAGAGGCTCAGAGACTCAGGTCCAGAGACTGACATATCTGACTCTGCTCCCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
DB 973 TTCAGCCGCTACTTCCATATGAGGGGCTCTGACTACACGCGCTGAGCCAGAGGTTC 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisThrLeuSer 360
DB 1033 ATCTGAGCTGTGTTAACAGACAGTGAATGCTGAGTGAAGCACTCCACACCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnAsnAspArgAlaThrGlnPro 380
DB 1093 GACACCTGTGGGAGACCTGTGATCTCTGCTTACAGCTGAACCTCCAGCGACGAGCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
DB 1153 TTGAATGGGCAAGATGAGGCTCTCTCCCTCGAGTGGGACAGACAGTCTCTCGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
DB 1213 GCTGAGCCAGTCCAGCTAAATCTCTGCTGCTGCTGTGACATCTTACCTGAGTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440

OY	341	lletpThrValPheAsnGlnThyValMetLeuSerAlaValGlnLeuHisThrLeuSer	360
Db	1033	ATCTGAGCATGCTGTAAACAGACAGTGAATGCTGAATGCTGAAGACAGCTCCACACCTTCCT	1092
OY	361	AspThrLeuTPGAlProGlyValAspSerArgLeuGlnLeuAnPheArgAlaThrGlnPro	380
Db	1093	GACACCCCTGTGGGGAGCTCGTGTACTCTGGCTACAGCTGAACCTTCGAGCAGACGAGCT	1152
OY	381	LeuAnGlyArgValAlleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla	400
Db	1153	TTGATATGGGCGAGTATGATGAGGCTCTCTTCCTGCTGGAGTGGAGACGAGTCTCGGCT	1212
OY	401	AlaGlnProValGlnLeuAnSerCysLeuAlaAlaGlyAspIleuValAlaPhe	420
Db	1213	GCTGAGCCAGTCCACACTGAATTCCTGCTGGCTGTGTCATCTCAATCCCTGGATTTT	1272
OY	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1273	GGCCCTCTTTTGTGCTGCTCACAGCCTCCGTTCTTGTGCAGATGAGAAGCAGACAGACA	1332
OY	441	ArgGlyThrIleuValGlyValSerThyArgProAlaGlnValAlaGlnThrGlyAla	459
Db	1333	AGGGGAACCAAGGGGGTGTAGACTACCGCCACGAGAGTACGCCGGAAGACTGGAGCC	1389

RESULT 12

US-08-260-190-5
Sequence 5. Application US/08260190A
Patent No. 6774117
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021-2
CURRENT APPLICATION NUMBER: US/08/260,190A
CURRENT FILING DATE: 1994-06-15
EARLIER APPLICATION NUMBER: 08/177,093
EARLIER FILING DATE: 1993-12-30
EARLIER APPLICATION NUMBER: 07/964,589
EARLIER FILING DATE: 1992-10-21
EARLIER APPLICATION NUMBER: PV-709-92
EARLIER FILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1522
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(1389)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (124)..(1389)
US-08-260-190-5

Alignment Scores:	
Pred. No.:	7 09e-202
Score:	2424.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	4
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 459
	Length: 1522

US-09-967-237A-2 (1-459) x US-08-260-190-5 (1-1522)

QY 1 MetLAPoleuCyPProSerPTrOTIpleuProleuLeuIleProLAProLAProGly 20
Db 13 ATGACGCCCTGTGCCCCAGCCCTGTGACTCCTCTGTGTATCCGGGCCCTGTGTCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
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Db	73	CTCATCTGTGCAACTGCTGTCATCAGTCTGCTTCTGATGCTGCTCCATCCACAGAGTTG	132
QY	41	ProATgMeGIngluIuAspSerProIeuGlyGlyIYSerSerGlyIuAspAspProIeu	60
Db	133	CCCCGGATGCAAGAGGATTCCTCCCTTGAGAGAGGCTCTTCTTGAGGAAGATGACCCACTG	192
QY	61	GlyGlyGluIuAspLeuProSerGlyIuIuAspSerProArgGluIuAspProProGlyIu	80
Db	193	GGCGAGGAGGATCTCCACAGTGAAGAGATTCCACAGAGAGAGATTCACCCGGAGAG	252
QY	81	GluAspLeuProGlyIuGluIuAspLeuProGlyIuGluIuAspLeuProGluValIYsPro	100
Db	253	GAGGATCTTACCTGGAGAGAGGATCTTACCTGGAGAGAGAGATTTACTGAACTTAAGCTT	312
QY	101	IYsSerGlyGluIuGlyIuGlyIYSerLeuIYsLeuGluAspLeuProThrValGluIuAProGlyI	120
Db	313	AAATCAGAAAGAGAGGGCTCCCTGAAAGTTAAGAGATCTACCTACTGTAGAGCTCTCGA	372
QY	121	AspProGIngluIuProGluIuAsnAsnAlaHisArgAspIYsGlyIuAspAspGInSerHis	140
Db	373	GATCTCTCAAGAACCCACAGATATATGCCCAAGGGAACAAAGAAAGGAGATGCCAGAGCAT	432
QY	141	TPAArgIYrGlyIuAspProProTrpProArgValSerProIaCysAlaGlyArgPhe	160
Db	433	TGGCCCTATGGAGGGACCCGCCCTGGGCCCGGGGTCTCCCACTGTGGCGGGCCGCTTC	492
QY	161	GInserProValAspIleArgProGInleuAlaIaPheCysProAlaIeuArgProIeu	180
Db	493	CAGTCCCGTGGAATTCGCCGCCACAGCTCGCGCTTCTGGCCGGCCCTGGCCCTCG	552
QY	181	GluIeuLeuGlyPheGInleuProProIeuProGluIuArgLeuArgAsnArgHis	200
Db	553	GAACTCTCGGGCTTCAGCTCCGCCGCTCCAGAACTCGCTCGGCAACAAATGGCCAC	612
QY	201	SerValGInleuThleuProProGlyIeuGluIuMerAlaIeuGlyIuProGlyIuArgGluIYr	220
Db	613	AGTGTCAACTGACCTTCCTCTGAGCTTGAAGATGGCTCTTGAGTCCCGGGCGAGACTAC	672
QY	221	ArgAlaIeuGInleuHisIleuHisIleuHisIleuHisIleuHisIleuHisIleuHisIleuHis	240
Db	673	CGGGCTCTGCACTGATTCGACATCGAGGGGCTGCAAGTCTGTCGGGGCTCGAGACACT	732
QY	241	ValGluGlyHisArgPheProAlaGluIuIleHisValIleHisIleuSerThralaPheAla	260
Db	733	GTTGGAAGGCAACGGTTTCCCTGCCGAGATCCACAGTGTTCACCTCAGACCGGCTTGGCC	792
QY	261	ArgValIaAspGluAlaIeuGlyIuArgProGlyIuGlyIuAlaIaValIeuAlaIaPheIeuGlu	280
Db	793	AGAGTTGACGAGGCTTGGGGCGCCCGGAGAGGCTGGCGTGTGGCCGCTTTCGGAG	852
QY	281	GluGlyIuProGluIuAsnSerAlaIYrGluIuIleuIeuSerArgIeuGluIuIleAla	300
Db	853	GAGGGCCCGGAGAGAAACAGTCCCTATGAGCAGTTCCTGCTCGCTTGGAGAAATGCT	912
QY	301	GluGluGlyIuSerGluIuThrGluIuProGlyIeuAspIleSerAlaIeuIeuProSerAsp	320
Db	913	GAGGAAGGCTCAGAGACTCAGGCTCCAGAGCATGGAATATCTGACCTCCGCTCGAC	972
QY	321	PheSerArgIYrPheGInIYrGluIuIYsIleuThrThrProProCysAlaGInGlyVal	340
Db	973	TTTACCCGCTTACCTTCAATATAGGGGTCTCTGACATCACCGCCCTGTGCCAGGGGTCTC	1032
QY	341	IleTPTrIuValPheAsnGInThrValMetLeuSerAlaIYsGInleuHisIleuThleuSer	360
Db	1033	ATCTGACTGTGTTTAACTCAGACAGTATGCTGAGTGTCTAAGCAGCTCCACACCTCTCT	1092
QY	361	AspThleuIuProGlyIuProGlyIuAspSerArgIeuGInleuAsnPheArgIaThrGInPro	380
Db	1093	GACACCTCTGTGGGACCTGTGACTCTGGGCTAACAGCTGAACCTCCGAGGAGACGAGCTT	1152
QY	381	LeuAsnGlyIuArgValIleGluIuAspPheProAlaGlyIuIaAspSerProAlaGlyIa	400
Db	1153	TTGATATGGGCGGATATGAGGCTTCCTTCCTGTGGAGTGAACAGAGTCTCGGGCT	1212


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? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CLO01307
? CURRENT APPLICATION NUMBER: US/09/949,016
? PRIOR APPLICATION NUMBER: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: PASTSEQ for Windows Version 4.0
? SEQ ID NO 4332
? LENGTH: 1552
? TYPE: DNA
? ORGANISM: Human
? US-09-949-016-4332

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; NAME/KEY: misc_feature
; LOCATION: (1) ..(5052)
US-08-260-190-23

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Score: 2233.00 Matches: 451
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Best Local Similarity: 97.62% Mismatches: 6
Query Match: 92.12% Indels: 8
DB: 4 Gaps: 0

US-09-967-237a-2 (1-459) x US-08-260-190-23 (1-5052)

QY 1 MetAlaProLeuCyPProSerProTPrLeuProLeuLeuIleProAlaProGly 20
DB 3545 ATGGCTCCCTGTCGCCAGCCCTGGCTCCCTGTGTGATCCGGCCCTGCTCCAGGC 3604
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 3605 CTCACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3664
QY 41 ProArgMetGlnGlnuAspSerProLeuGlyGlyGlySerSerGlyGlyuAspAspProLeu 60
DB 3665 CCCCGATGACAGAGGATTC-CCCCCTGGAGAGGCTCTTCTGGGAAAGATGACCCACTG 3723
QY 61 G1yGluGlnuAspLeuProSerGluGluuAspSerProArgGluGluAspProGlyGlyu 80
DB 3724 GCGGAGAGGATCTGCCCACTGAGAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 3783
QY 81 GlnuAspLeuProGlyGlyGluuAspLeuProGlyGlyGluuAspLeuProGluValLys-Pr 100
DB 3784 GAGGATCTACCTGGAGAGAGGATCTACCTGAGAGAGAGGATCTACCTGAAGTTAATGCC 3843
QY 100 oLysSerGluGlnGluGlySerLeuLysLeuGluuAspLeuProThrValGlnuAspProGly 120
DB 3844 TAAATCAGAAAGAGAGGATCTCCCTGAAAGTTAGAGGATCTACCTGTTGAGGCTCTGG 3903
QY 120 YAspProGlnGluProGlnuAsnAsnAlaHisArgAspLysGluGlyuAspAspGlnSerHis 140
DB 3904 AGATCCCTCAGAGAACCCAGAAATATGCCACAGGAGCAAGAGGATGACCAAGTCA 3963
QY 140 sTTPArgTYrGlyGlyuAspProProTTPProArgValSerProAlaCySalaglyArgph 160
DB 3964 TTGGCGCTATGAGGACACCGGCC-TCGGCCCGGGGTCTCCCAAGCTGCGGGCCGCTT 4022
QY 160 eGlnSerProValAspLysArgProGlnuAsnAlaAlaPheCySerProAlaLeuArgProLe 180
DB 4023 CCAGTCCCCGGTGATATCCGCCCCCAAGCTGCGCCTTCTGCCCCGGGCCCTGCCCT 4082
QY 180 uGluLeuLeuGlyPheGlnLeuProProLeuProGlnuLeuArgLeuArgAsnAnglyHis 200
DB 4083 GGAACTCTGGGCTTCCAGCTCCCGCGCTCCCAAGCTGGGCTGCA-GACAAATGGCCA 4141
QY 200 sSerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyuTy 220
DB 4142 CAGGTGCAACTGACCTGCTCTCGGGCTAGAGATGCTCTGGGTCCCGGGCGGAGTA 4201
QY 220 rArgAlaLeuGlnLeuHisLeuHisSTrPGlyAlaAlaIleArgProGlySerGlyuHisSTH 240
DB 4202 CCGGCT-CTGAGCTGATGCTGCACTGGGGGGCTGCAAGTGTCTCGGGCTCGAGCACAC 4260
QY 240 rValGluGlyHisArgPheProAlaGluIleHisValValHisSerSerThrAlaPheAl 260
DB 4261 TTGGGAAGGCCACCGTTTCCCTGCCAGATCCAGTGTTCACCTCAGCACCGCTTTGC 4320
QY 260 aArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValIleuAlaAlaPheLeuGly 280
DB 4321 CAGAGTTGACGAGGCTTTGGGGCGCCCGGAGGAGCTGGCGCTGTGGC-GCCTTTCTGGA 4379
QY 280 uGluGlyProGlnGluuAsnSer-AlaTyrgluGlnuLeuLeuSerArgLeuGluGluIleA 300
DB 4380 GGAAGGCCCCGGAAGAAACAAGTCTTATGAGCAGTTGCTGTCTGCTTGGAGAAATCG 4439

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QY 300 laGluGluGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerA 320
DB 4440 CTGAGGAGGCTCAGAGACTCAGCTCCAGGACTGGACATATCTGACCTCTGCCCTCTG 4499
QY 320 sPheSerArglyrPheGlnTYrGlyGlySerLeuThrThrProProCyAlaGlnGly 340
DB 4500 ACTTCAGCCCTCTTCCAAATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGAGGTG 4559
QY 340 aLleTPThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisSTHLeuS 360
DB 4560 TCATCTGAGCTGTGTTTAACCAACAGATGCTGAGTGTAGGAGCTTACACCTCT 4619
QY 360 eAspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnP 380
DB 4620 CTGACACCTGTGGGAGCTGTGACTCTGCTACAGCTGAACCTCCAGCGACGACG 4679
QY 380 rLeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValaAspSerSerProArgA 400
DB 4680 CTTTGAATGGCGAGATGATGAGGCTCTCCCTGCTGAGTGGACAGCAGCAGCTCGGG 4739
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QY 420 heGlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisA 440
DB 4800 TTGGCCCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4859
QY 440 rArgArglyrThrLysGlyValSer-TyrArgProAlaGluValaAlaGluThrArgAla 459
DB 4860 GAAAGGGAACCAAGGGGGGTGAGGCTTACCGCCAGAGGATGACCGAGACTGGAGCC 4919

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Search completed: August 20, 2005, 01:29:39
 Job time : 275 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 21:25:55 ; Search time 4549 Seconds
(without alignments)
3840.734 Million cell updates/sec

Title: US-09-967-237a-2

Perfect score: 2424
Sequence: 1 MAPLCBPWMLILIPAPAG.....RRGTGGSVRAVAETGA 459

Scoring table:

BLOSUM62
Xgapop 10.0 , Ygapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUPPLX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

EST:
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2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
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6: gb_est5.*
7: gb_est6.*
8: gb_gse81.*
9: gb_gse82.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2420	99.8	1469	3	CR616345 full-leng
2	2420	99.8	1523	3	CR620502 full-leng
3	2420	99.8	1541	3	CR597234 full-leng
4	2361.5	97.4	1492	3	CR590646 full-leng
5	1790	73.8	1084	1	AL542336
6	1567	64.6	1070	1	AL554705
7	1556.5	64.2	1009	1	AL558378
8	1501.5	61.9	1017	5	AL558378
9	1472	60.7	916	5	BX423970

10	1452.5	59.9	971	7	COS79387
11	1401	57.8	927	1	AL555184
12	1332	55.0	1071	1	AL554665
13	1304.5	53.8	874	4	BG386425
14	1211	50.0	836	5	BX383092
15	1130	46.6	740	7	CR971835
16	1121	46.2	1017	1	AL580216
17	1115	46.0	994	1	AL577748
18	1114	46.0	668	4	BG824243
19	1113	45.9	818	2	BE548062
20	1092	45.0	782	2	CR696500
21	1090	45.0	761	5	BX423969
22	1075	44.3	722	1	CR978804
23	1064.5	43.9	746	4	BI232323
24	1060.5	43.8	806	2	BE344769
25	1041	42.9	589	4	BM790508
26	1041	42.9	813	7	CO734371
27	1002.5	41.4	736	2	BE543633
28	989	40.8	830	7	CR849799
29	986.5	40.7	945	7	CF579370
30	965	39.8	715	7	CR63805
31	945.5	39.0	649	6	BY735107
32	940	38.8	717	2	AW701559
33	932	38.4	709	7	CR65416
34	919.5	37.9	733	4	BG819731
35	910	37.5	682	1	AI831707
36	904	37.3	689	1	CA425935
37	886	36.6	551	6	CA406362
38	886	36.6	691	5	BU620600
39	879	36.3	502	7	CV029038
40	877.5	36.2	795	2	AW083555
41	862	35.6	668	7	CR62471
42	851	35.1	669	1	AI925646
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44	836	34.5	658	1	AI769526
45	830.5	34.3	582	4	BI534892

ALIGNMENTS

RESULT 1
CR616345
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
FEATURES
source

CR616345
full-length cDNA clone CSODA003YB12 of Neuroblastoma of Homo sapiens (human).
CR616345
CR616345.1 GI:50497152
HTC; CNSLT CDNA.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1469)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1469)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. 1469
/organism="Homo sapiens"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA003YB12"
/tissue_type="Neuroblastoma"
/plasmid="pCMVSPORT_6"

Alignment Scores:

Pred. No.: 2,44e-185 Length: 1469
Score: 2420.00 Matches: 458
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.83% Indels: 0
DB: 3 Gaps: 0

US-09-967-237A-2 (1-459) x CR616345 (1-1469)

QY 1 MetAlaProLeuCyPProSerProTTPLeuProLeuLeu1LeProAlaProGly 20
Db 5 ATGGCTCCCTGGCCAGCCCTGGCTCCCTGTGATCCCGGCCCTGCTCCAGGC 64
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 65 CTCACTGTGAACTGCTGCTGTCTCTGCTTGTGCTGTCTCTCACTCCCGAGAGTTG 124
QY 41 ProArgKetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
Db 125 CCCCGAGTGCAGAGAGATCCCTCCCTGGAGAGAGCTCTTGCGGGAATGACCCACTG 184
QY 61 GlyGluGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db 185 GGGGAGAGAGATCTGCCAGTGAAGAGATTCACCGAGAGAGAGATCCACCCGAGAG 244
QY 81 GlnAspLeuProGlyGlnGluAspLeuProGlyGlyGluGluAspLeuProGlyValIysPro 100
Db 245 GAGGATCTACTGAGAGAGAGATCTACTGAGAGAGAGATCTACTGTTGAGAGCTCTGGA 304
QY 101 LysSerGlnGluGlnGlySerLeuLysLeuGlnAspLeuProThrValGluAlaProGly 120
Db 305 AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTTGAGAGCTCTGGA 364
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
Db 365 GATCTCTCAAGAACCCCGAATTAAGCCACAGAGGACAAAGAGGATGACCAAGATCAT 424
QY 141 TrpArgTyrglyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
Db 425 TGGCGCTATGAGAGCGACCCGCTGAGCCCGGGGTGTCCCGAGCTGCGGGCGGCTTC 484
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCyPProAlaLeuArgProLeu 180
Db 485 CAGTCCCGGCTGATATCCGCCCACTGCGCGCTTGCCTGCCGCGCTGCCGCGCTG 544
QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlyHis 200
Db 545 GAATCTCTGGAGCTTCAGCTCCGCGCTCCCAACTGGCGCTGCGCAACAATGGGCAC 604
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Db 605 AGTGTGAACTGACCCCTGCTCCGAGCTAGAGATGCTCTGGGTCCCGGGCGGAGATAC 664
QY 221 ArgAlaLeuGlnLeuHisLeuHisIleTyrglyAlaAlaGlyArgProGlySerGlnHisThr 240
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QY 241 ValGlnGlyHisArgPheProAlaGluIleHisValValHisLeuSerTrpAlaPheAla 260
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QY 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
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QY 281 GlnGlyProGlnGluAsnSerAlaTyrglnLeuLeuSerArgLeuGlnGluIleAla 300
Db 845 GAGGAGCCCGGAAAGAAACAGTGCCTATGAGCACTGCTGCTGCTGGAAGAAATGCTT 904
QY 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 905 GAGGAAGCTCAAGACTCAGGTCCAGAGCTGAGCATATCTACCTCCGCGCTCTGAC 964
QY 321 PheSerArgTyrgPheGlnTyrgGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 965 TTCAACCGCTACTCTCAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTCTC 1024
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisIleThrLeuSer 360
Db 1025 ATCTGAGTGTGTAACTCAAGACATGATGCTGATGCTGAAGCAGCTCCACACCTCTCT 1084
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1085 GACACCTGTGGAGACTGTGACTCTCGGCTACGCTGAACCTTCGAGCGACAGACCTT 1144
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1145 TTGAATGGCGGAGATGATGAGGCTCTCTCTCTGCTGAGTGGACAGCACTCCGGGCT 1204
QY 401 AlAGlnProValGlnLeuAsnSerCyLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1205 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1265 GGCTCTCTTTCTGTGCTACACAGCTGCTGCTCTCTCTGTCAGATGAGAAAGCGACACA 1324
QY 441 ArgGlyThrLysGlyGlyLysTyrgArgProAlaGluValAlaGlnThrGlyAla 459
Db 1325 AGGGAACCAAGAGGGGTGTGACTACCGCCGACAGAGAGTACCGAGATGGAGGCC 1381

RESULT 2
CR620502
LOCUS
DEFINITION
Full-length cDNA clone CS0DK007YK10 of Hela cells Cot 25-normalized
of Homo sapiens (human).

ACCESSION
CR620502.1 GI:50501309
VERSION
HTC; CDS; CDS; CDS
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
Contact: Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Barclay Avenue
2 (bases 1 to 1523)
Genoscope.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1523
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK10"
/tissue_type="Hela cells Cot 25-normalized"

Pred. No.: 2.6e-185 Length: 1541
 Score: 2420.00 Matches: 458
 Percent Similarity: 100.00% Conservation: 1
 Best Local Similarity: 99.78% Mismatches: 0
 Query Match: 99.83% Indels: 0
 DB: 3 Gaps: 0

US-09-967-237a-2 (1-459) x CR597234 (1-1541)

QY 1 MetAlaProLeuCySPoSerProTriPLeuProLeuLeuIlePProAlaProGly 20
 Db 42 ATGGCTCCCTGTCGCCCCAGCCCCCTGGCTCCCTGTTGATCCGCCCCCTGCTCCAGGC 101
 QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
 Db 102 CTGACTGTGAACTGCTGTGTACTGCTGCTGCTGTGTGTGCTGTCCATCCCAAGAGTTG 161
 QY 41 ProArgMetGlnLeuAspSerProLeuGlyGlySerSerGlyLeuAspAspProLeu 60
 Db 162 CCCCGATGACAGAGGATTCCTCCCTGGAGAGGCTTCTGGGGAAGATGACCCACTG 221
 QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProGlyGlu 80
 Db 222 GCGCAGAGGATCTGCCAGTGAAGAGATTCCACCAAGAGAGATCCACCCGAGAG 281
 QY 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlyGlnGluAspLeuProGlyValysPro 100
 Db 282 GAGGATCTACTGGAGAGAGGATCTACTGAGAGAGAGATCTAAGTTAAAGCT 341
 QY 101 LysSerGlnGlnGlnGlySerLeuLeuGlnGluAspLeuProThrValGlnAlaProGly 120
 Db 342 AAATTCAGAAAGAGGGCTCTCTGAAATTAGAGATCTACTGTTGAGGCTCTGGA 401
 QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
 Db 402 GATCTTAAAGAACCCCGAATTAATGCCCAAGAGACAAAGAGGATGACACAGATCAT 461
 QY 141 TyrArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
 Db 462 TGGGGCTATGAGAGCGACCGCCCTGGAGCCCGGGGTGCCAGGCTCGCGGGCGCTTC 521
 QY 161 GlnSerProValAspLeuArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
 Db 522 CAGTCCCGGTGATATCCGCCCACTGCGCCCTTGTGCCCGGCGCTCGCGCCCTG 581
 QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnGlnHis 200
 Db 582 GAATCTCTGGGCTTCCAGCTCCGCCCTCCAGAACTGGCGCTGGCCCAATGGCCAC 641
 QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyTyr 220
 Db 642 AGTGTGCAATGACCTGCTCTCCCTGGGCTAGAGATGAGCTCGGGTCCCGGAGGAGTAC 701
 QY 221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaAlaAlaGlyArgProGlySerGlnHisThr 240
 Db 702 CGGGCTCTGAGCTGCACTGTGCACTGGGGGCTGCACTGCTCGGGCTCGGAGCAACT 761
 QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisValValHisLeuSerThrAlaPheAla 260
 Db 762 GTGGAAGGCAACCTTCTCCCTGCGAGATCCAGCTGTTCACTCAGACACCGCTTTGCC 821
 QY 261 ArgValAspGlnAlaLeuGlyArgProGlyLeuAlaValLeuAlaAlaPheLeuGln 280
 Db 822 AGAGTTGACAGGCTTGGGGCGCCCGGAGAGCTGCGCTGTGGCGCGCTTTCTGGAG 881
 QY 281 GlnGlyProGlnGlnAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
 Db 882 GAGGGCCCGGAAGAAACAGTGTGCTATGAGAGTGTGTGCTGTGGAAAGATGCT 941
 QY 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
 Db 942 GAGGAAGGCTCAAGACTCAGGTCCCAAGACTGAGCAATATCTGACTCTGCGCTCTGAC 1001

QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
 Db 1002 TTCAGCCGCTACTTCCAAATATGAGGGGTCTGTGACTACACCGCCCTGTGCCAGGGTGC 1061
 QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisTyrLeuSer 360
 Db 1062 ATCTGACTGTGTTTAAACAGACAGATGATGTAGTGTCTAAGAGCTCCACACCTCTCT 1121
 QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
 Db 1122 GACACCTGTGGGAGACTGTGACTCTCGGCTACAGCTGAATCTCCAGAGGAGAGAGCT 1181
 QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerProArgAla 400
 Db 1182 TTGAATGGCGAGATGATTGAGGCTCTCTCCCTGTGAGTGAACAGACTCCCTCGGCT 1241
 QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
 Db 1242 GCTGAGCACTCCAGCTGAATTCCTGCTGGCTGGTGTGACATCTTACGCCCTGTGTTT 1301
 QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
 Db 1302 GGCCTCTTTTCTGTGTGACCAAGCTGCTGCTTCTGTGAGATGAGAAAGCAGACAGA 1361
 QY 441 ArgGlyThrLysGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
 Db 1362 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGAGGCC 1418

RESULT 4

CR590646 1492 bp mRNA linear HTC 21-JUL-2004
 LOCUS full-length cDNA clone CS0D005YK14 of T cells (Jurkat cell line)
 DEFINITION Cot 10-normalized of Homo sapiens (human).
 CR590646
 ACCESSION CR590646.1 GI:50471453
 VERSION HTC; CDS1T_CDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1492)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/InvitrogenCorporation 1600
 Faraday Avenue
 2 (bases 1 to 1492)
 REFERENCE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.

FEATURES location/Qualifiers
 source 1..1492
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D005YK14"
 /tissue_type="T cells (Jurkat cell line) Cot
 10-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
 Pred. No.: 1.36e-180 Length: 1492
 Score: 2351.50 Matches: 449
 Percent Similarity: 98.04% Conservation: 1

Best Local Similarity: 97.82% Mismatches: 0
 Query Match: 97.42% Indels: 9
 DB: 3 Gaps: 1

US-09-967-237a-2 (1-459) x CR590646 (1-1492)

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Qy 1 MetAlaPLeuCyPProSerProTrpLeuProLeuLeuLeuProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTTGATGCCGCCCTGCTCAAGC 102
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACCTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162
Qy 41 ProArgMetGlnGlnuAspSerProLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 60
Db 163 CCCCAGAGAGAGAGAGATTTCCCTTGGAGAGAGGCTCTTCTGGGAGAGATACCCACTG 222
Qy 61 GlnGlnGlnuAspLeuProSerGlnGlnuAspSerProArgGlnGlnuAspProGlnGln 80
Db 223 GCGGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCCGAGAG 282
Qy 81 GlnuAspLeuProGlnGlnuAspLeuProGlnGlnuAspLeuProGlnuValuAspPro 100
Db 283 GAGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCTGAAGTTAAGCT 342
Qy 101 LysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 120
Db 343 AAATCAGAGAGAGAGAGGCTCCCTGAGATTAGAGATCTACCTGAGAGGCTCTGGA 402
Qy 121 AspProGlnGlnuProGlnuAsnAsnAlaHisArgAspLysGlnGlnuAspAspGlnSerHis 140
Db 403 GATCTCAAGAAACCCCAATATATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 462
Qy 141 TrpArgTrpGlnGlnuAspProProTrpProArgValSerProAlaCysAlaGlnArgPhe 160
Db 463 TGGCGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
Qy 161 GlnSerProValAspLysArgProGlnuLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCGGTGAGATATCGGCCCCAGGCTCGGCTTCTGCCCCGCTGCGCCCCCTG 582
Qy 181 GlnuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 200
Db 583 GAATCTCCGAGCTTCAAGCTCCGCGCTCCCAAGATCGCGCTGCGCAACATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlnGlnuLeuMetAlaLeuGlnGlnGlnGlnGlnGln 220
Db 643 AGTGTGCAACTGACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlnValAlaGlnArgProGlnGlnGlnGlnGlnGln 240
Db 703 CGGGCTCTGAGAGCTGATCTGCACTGGGGGGGTGAGGCTGCGCGCTGCGAGACACT 762
Qy 241 ValGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 260
Db 763 GTGAGAGGCAACGCTTCCCTGCGAGATCCAGTGTCTACCTACAGACCGCCCTTGGC 822
Qy 261 ArgValAspGlnuAlaLeuGlnArgProGlnGlnuAlaValLeuAlaAlaPheLeuGln 280
Db 823 AGAGTTGACGAGAGCTTGGGGGGGCGGGAGGCGCTGGCGCTTGGCGCTTCTGAG 882
Qy 281 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 300
Db 883 GAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 942
Qy 301 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 320
Db 943 GAGAGAGGCTCAAGAGACTCAAGTCCAGAGACTGAGACATCTGCACTCTGCTCTGAC 1002
Qy 321 PheSerArgTrpPheGlnTrpGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 340
Db 1003 TTCAGCGCGCTACTTCAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1062

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Qy 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1063 ATCTGAGCTGTGTATTACCAACAGACTGATGCTGAGCTGTAAGCACTCAACCCCTCTCT 1122
Qy 361 AspThrLeuTrpGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 380
Db 1123 GACACCCCTGTGGGAGCCTGTGAGACTCTGCGGTACAGCTGAAGCTTCCGAGCGAGCCT 1182
Qy 381 LeuAsnGlnArgValIleGlnuAlaSerPheProAlaGlnValAspSerSerProArgAla 400
Db 1183 TTGAATGGCCAGAGATGAGAGGCTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1242
Qy 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaGlnAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCCA-----GGTGAACCTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1275
Qy 421 GlnLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1276 GGCCTCTTTTGGCTGTCACAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1335
Qy 441 ArgGlnTrpLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 459
Db 1336 AGGGAGACCAAGGGGGGTGAGCTACCGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1392

RESULT 5
AL542336 1084 bp mRNA linear EST 24-MAR-2004
LOCUS AL542336 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YB19
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION AL542336
VERSION AL542336.3 GI:45717912
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1084)
AUTHORS Li, W.B., Gruber, C., Jessup, J., and Polayars, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:30547384.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 8734.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0DE010CA10Q2&c=8734.f.
FEATURES
source
1..1084
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE010YB19"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Alignment Scores: 1.64e-134 Length: 1084
Pred. No.: 1790.00 Matches: 337
Score: 1790.00 Conservative: 4
Percent Similarity: 97.99%

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Best Local Similarity: 96.84%      Mismatches: 6
Query Match:          73.84%      Indels: 1
DB:                  1            Gaps: 0
US-09-967-237A-2 (1-459) x AL542336 (1-1084)

QY      3 ProLeuCySPSerProTTPLeuProLeuLeu1leProAlaProAlaProGlyLeuThr 22
DB      29 CCCCTGTGCCCCAGACCCCTGGCTCCCTGTGTGATCCCGGCCCTGCTCCAGGCTCACT 88
QY      23 ValGlnLeuLeuLeuSerLeuLeuLeuMeCProValHisProGlnaArgLeuProArg 42
DB      89 GTGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148
QY      43 MetGlnLeuAspSerProLeuGlyGlyGlySerSerGlyGlyAspAspProLeuGlyGlu 62
DB      149 ATGAGAGAGATTCCTCCCTTGAGAGAGAGCTCTTCTGGAGAAAGTATGACCACTGGGAG 208
QY      63 GluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlyGluAsp 82
DB      209 GAGGATCTGCCCACTGTAAGAGGATTCACCCAGAGAGAGGATCCACCCGGAGAGAGAT 268
QY      83 LeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyValLeuProGlySer 102
DB      269 CTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGATTAAGCTTAATAATCA 328
QY      103 GlnGlnGlnGlySerLeuLeuGlyLeuGluAspLeuProThrValGlnAlaProGlyAspPro 122
DB      329 GAAGAAGAGGCTCCCTCGAAGTTAGAGATTTACTTACTGTTGAGGCTCTCGAGAGATCCT 388
QY      123 GlnGlnProGlnaAsnAlaHisArgAspGlyGlnGlyAspAspGlnSerHisTTPArg 142
DB      389 CAAGAACCCAGATTAATGCCCACAGAGAGCAAAAGAGAGATGACAGAGATCTTGGCGC 448
QY      143 TygGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPheGlnSer 162
DB      449 TATGAGAGCGACCCGCTGGCCCGGAGTGTCCACAGCTGGCGGGCGGCTTCAGTCC 508
QY      163 ProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuAspProLeuGlnLeu 182
DB      509 CCGGTGATATCCGCCCCCAGACTCGCGCTTGGCCCGGCGCCCTCGGAATC 568
QY      183 LeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgaAsnAnglyHisSerVal 202
DB      569 CTGGGCTTCAGACTCCCGCGCTCCAGAACTGGCGCTGCGCAAAATGGCGCACAGTGTG 628
QY      203 GlnLeuThrLeuProProGlyLeuGlnMeCAlaLeuGlyProGlyArgGlyuTYRArgAla 222
DB      629 CAACGTACCTGCTCTCGGCTAGAGATGCTGTGGGTCCCGGCGAGATACCGGACT 688
QY      223 LeuGlnLeuHisLeuHisTTPGlyAlaAlaGlyArgProGlySerGlnHisTTPValGlu 242
DB      689 CTGAGCTGATCTGCACTGGGGGGCTGCAAGTGTCTCGGGCTCGAGACACACTGTGAA 748
QY      243 GlyHisArgPheProAlaGluHisValValHisLeuSerThrAlaPheAlaArgVal 262
DB      749 GGGTACCGTTTCCCTGCGAGATCCACGTGGTTCACCTCAGCACCGGCTTTCAGAGATT 808
QY      263 AspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlnGlnGly 282
DB      809 GACAGAGCTTGGGGCGCCCGAGAGGCTGGCCGTGTGGCGGCTTTCGAGAGAGGCG 868
QY      283 ProGlnGlnaSerAlaTYRLeuGlnLeuLeuSerArgLeuGlnGluAlaGlnGlu 302
DB      869 CCGGAAGAAAACAGTGTCTATGACAGATTTGCTGTCTTGGAGAAATGCTGAGAGAA 928
QY      303 GlySerGlnThrGlnValProGly-LeuAspIleSerAlaLeuLeuProSerAspPheSe 322
DB      929 GGCTCAAGAGACTCAGTCCAGGACTTGACATATCTKSACTCTGSCCTCTGACTTCAG 988
QY      322 TATGTYRPhGlnThrGlnGlySerLeuThrThrProProCysAlaGlnGlyValIleTYR 342
DB      989 CCGCTACTTCAAAATATAGAGGGGCTGTGACTACACCGCCCTGTGKGCAGAGGTGTCACTK 1048

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QY      342 ptnValPheAsnGlnThrVal 349
DB      1049 GACTGTGTTTAAACAGMAGT 1070

RESULT 6
AL554705
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5300.F
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSOD1085YF1&c=5300.F.

FEATURES
source
location/Qualifiers
1..1070
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1085YF18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 1.84e-116 Length: 1070
Score: 1567.00 Matches: 318
Percent Similarity: 92.53% Conservative: 4
Best Local Similarity: 91.38% Mismatches: 22
Query Match: 64.65% Indels: 8
DB: 1 Gaps: 2

US-09-967-237A-2 (1-459) x AL554705 (1-1070)

QY      1 MetAlaProLeuCySPSerProTTPLeuProLeuLeu1leProAlaProAlaProGly 20
DB      42 ATGGCTCCCTGTGCCCCCAGACCCCTGGCTCCCTGTGTGATCCCGGCCCTGCTCCAGGC 101
QY      21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMeCProValHisProGlnaArgLeu 40
DB      102 CTACAGTGTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 161
QY      41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGlyAspAspProLeu 60
DB      162 CCGCGATGACAGAGAGATTCCTCCCTTGAGAGAGGCTCTTCTGGAGAAAGTATGACCACTG 221
QY      61 GlnGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
DB      222 GGGAGAGAGATCTGCCCACTGTAAGAGATTTCACCCAGAGAGAGATTCACCCCGAGAGAG 281

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Db 523 CAGTCCCGGTGATATCCGCCCCAGCTCGCGCTTTCGCCGCGCTTCGCGCCCTCG 582
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuAArgLeuAAsenGlyHis 200
Db 583 GAATCTCTGGGCTTCCAGCTCCGCGCTCCAGAACTGGCGCTGGCAACATAGGCGAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyAArgGlyTyr 220
Db 643 AGTGTGCACATGACCCCTGCTCCCTGGGCTAGAGATGCTGTGGGTCCCGGCGGAGTAC 702
Qy 221 AArgAlaLeuGlnLeuHisLeuHisSTrPGlyAlaAlaGlyAArgProGlySerGlyHisThr 240
Db 703 CGGGCTCTGAGCTGCACTGCACTGGGAGGAGCTGCAAGTGTCTCGGAGCTGGAGCAACT 762
Qy 241 ValGlnGlyHisAArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAGAGCCACCGTTTCCCTGCGAGATCCAGCTGTTCACCTCGACACCGCTTTGCC 822
Qy 261 AArgValAspGluAlaLeuGlyAArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTGACAGAGCTTGGGCGCGCCCGGAGAGCTGTGGTGGC-GCCTTCTGGAG 881
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGluLeuLeuSerAArgLeuGluGluLeuAla 300
Db 882 GAGGSCCGGAAGA-AAAGTGTCTATGAGAGAGTGTCTGTCTGCTTGGAAARA-ATGCT 939
Qy 301 GluGlnGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuPro 318
Db 940 GAGGAAGC-TCAGAGACTCAGKCCAGACTGGACAMATT-GCAGCTCGGCT 991
RESULT 8
BX401186 1017 bp mRNA linear EST 29-APR-2004
LOCUS BX401186 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.
BX401186
ACCESSION BX401186.2 GI:46876709
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 1017)
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Mammalian: Eutheria; Primates; Catarrhini; Homnidae; Homo.
COMMENT On May 13, 2003 this sequence version replaced gi:30626393.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?S=CS0DK009DH05QP1c=5300.f.
location/Qualifiers
1.1017
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK009YP10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA
was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 3,44e-111 Length: 1017
Score: 1501.50 Matches: 290
Percent Similarity: 92.99% Conservative: 2
Best Local Similarity: 92.36% Mismatches: 19
Query Match: 61.94% Indels: 4
DB: 5 Gaps: 3
US-09-967-237a-2 (1-459) x BX401186 (1-1017)
Qy 3 ProLeuCyPProSerProTTPLeuProLeuLeuIleProAlaPProAlaPProGlyLeuThr 22
Db 19 CCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTATCCCGCCCCCTGCTCAGGCTTCACT 78
Qy 23 ValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnAArgLeuProAArg 42
Db 79 GTGCACTGCTGTGCTGCACTGCTGCTTGTGTGTCTGTCCATCCCGAGAGTTGCCCG 138
Qy 43 MetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeuGlyGlu 62
Db 139 ATCAGAGAGGATTCCTCCCTTGGAGAGGCTTCTTGGGAGATGATCACCAGTGGCGAG 198
Qy 63 GluAspLeuProSerGluGluAspSerProAArgGluGluAspProGlyGlyGluAsp 82
Db 199 GAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCCGAGAGAGAT 258
Qy 83 LeuProGlyGlyGluGluAspLeuProGlyGlyGluGluAspLeuProGlyGlySer 102
Db 259 CTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGATTAAGCTTAATCA 318
Qy 103 GluGlnGlyGlySerLeuLeuGluAspLeuProThrValGluAlaProGlyAspPro 122
Db 319 GAAGAAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTAGAGCTCTGAGAGATCT 378
Qy 123 GluGluProGlnAsnAsnAlaHisAArgAlaGlyGlyAspAspGlnSerHisSTrPArg 142
Db 379 CAAGAACCAGATATATGCCCAAGAGCAAAAGAGGATACCAAGATCATTTGGCGC 438
Qy 143 TyrGlyGlyAspProProTTPProAArgValSerProAlaCysAlaGlyAArgPheGlnSer 162
Db 439 TATGAGAGCGACCCGCTGCGCCCGGAGTGTCCCGAGCTGCGCGCGCTTCCAGTCC 498
Qy 163 ProValAspIleAArgProGlnLeuAlaAlaPheCysProAlaLeuAArgProLeuGluLeu 182
Db 499 CCGGTGATATCCGCCCCAGCTCGCGCTTGTGCGCGCCCTGCGGCCCTCGGAATC 558
Qy 183 LeuGlyPheGlnLeuProProLeuProGluLeuAArgAsnAsnGlyHisSerVal 202
Db 559 CTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGGCAACATGCGCAAGTGTG 618
Qy 203 GlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyAArgGlyTyrAArgAla 222
Db 619 CACTACACCTGCTCTCTGGGCTAGAGATGCTCTGGTCCCGGGGGAGTACCGGGCT 678
Qy 223 LeuGlnLeuHisLeuHisSTrPGlyAlaAlaGlyAArgProGlySerGlyHisThrValGlu 242
Db 679 CTCAGCTGATCTGCACTGGGAGGCTGCAAGTGTCTCGCGGCTCGAGAGACACTGTGGA 728
Qy 243 GlyHisAArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAlaArgVal 262
Db 739 GGCACCGTTCCTCTCGCGAGTCAAGTGTTCACCTCAGCACCGCTTGGCAAGATT 798
Qy 263 AspGluAlaLeuGlyAArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGluGly 282
Db 799 GAGGAGCGCTTGGGAGCGCGGAGAGCTG-GCGGTGTGGCGCTTCTGAGAGAGG--- 854
Qy 283 ProGlnGluAsnSerAlaTyrGluGlnLeuLeuSerAArgLeuGluGluLeuAlaGlyGlu 302
Db 855 CCGGGAAGAAACAGTCTTATGAGAG--TTGTGTCTGCTGGGAAATCGCTGAGGAA 911
Qy 303 GlySerGluThrGlnValProGlyLeuAspIleSerAlaLeu 316
||| :||| ||||| |||

Db 912 GGT---CAGAGMTCAAGTCCAGACCTGAGMTATYTCVTTCTG 950

RESULT 9
BX423970 916 bp mRNA linear EST 03-MAY-2004
LOCUS BX423970 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CS0DA003YB12 5-PRIME, mRNA sequence.
ACCESSION BX423970 GI:46955310
VERSION BX423970.2 GI:46955310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30766328.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna7s-CS1DA001ZFP09QPI&c=5300.f.

FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA003YB12"
/cissue_type="NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7,29e-109 Length: 916
Score: 1472.00 Matches: 276
Percent Similarity: 92.43% Conservative: 5
Best Local Similarity: 90.79% Mismatches: 23
Query Match: 60.73% Indels: 0
Gaps: 0

US-09-967-237a-2 (1-459) x BX423970 (1-916)

QY 1 MetAlaProLeuCySProSerProTrieuProLeuLeu1leProAlaProAlaProGly 20
Db 5 ATGGCTCCCTGTGCTCCCGACGCCCTGCTGCTGTGTAACCGCGCCCTGCTCCAGGC 64
QY 21 leuThrAlaGlnleuLeuLeuSerleuLeuLeuMetProValHisProGluAlaArgleu 40
Db 65 CTCACCTGGCAACMGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 125 CCCCGAGTGCAGAGGAGATTCCCTTGGGAGAGGCTCTWCTGGGGAAGATGACCACTG 184
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProAlaGluGluAspProGlyGlu 80
Db 185 GGCAGAGGAGATGCTGCCAGTGAAGAGATTCAACCAAGAGAGATCCACCGGAGAG 244
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValIysPro 100

Db 245 GAGGATCTACTGGAGAGAGGAGATCTACTGGAGAGGAGATCACTGAAGTAAAGCT 304
QY 101 LysSerGluGluGluGlySerLeuLeuGluAspLeuProThrValGluAlaProGly 120
Db 305 AAATCAGAGAGAGAGGCTCTCTGATAGAGATCTACTGTTGAGGCTCTGGA 364
QY 121 AspProGlnGluProGluAspAsnAlaHisArgAspLysGluGluAspAspGlnSerHis 140
Db 365 GAACCTCAAGAACMCACGAATAMGCCACAGGACAAAGAGAGATGACCAAGTCA 424
QY 141 TrpArgTyrGlyGlyAspProProTrieuProAlaSerProAlaCyAlaGlyArgPhe 160
Db 425 TGGCGCATGAGAGCGACCCGCCCTGGCCCGGGTGTATCCAGAGCTGGGGCGCTTC 484
QY 161 GlnSerProValAspLleArgProGlnLeuAlaAlaPheCyAspProAlaLeuArgProLeu 180
Db 485 CAGTCCCGGGTGTATATCCGCCGCCACAGCTGCGCCCTTGTGCGCGGCTTGGCCCTG 544
QY 181 GluLeuLeuGlyPheGlnLeuProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 545 GAACCTCTGGGCTTCCAGCTTCCGCCCTCCAGAACCTGGCTGGCMACATGGCCAC 604
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 605 AGTGTGACACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 664
QY 221 ArgAlaLeuGlnLeuHisAlaLeuHisTyrGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 665 CGGCTCTGACAGCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 724
QY 241 ValGluGlyHisArgPheProAlaGluLleHisValAlaHisLeuSerThrAlaPheAla 260
Db 725 GTGTAAGCCACCGCTTCCGCGGAGATCCAGTGTATCTARACACCGCTTTC 784
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 785 ARATTTGAMAGAGGCTTGGGGCGCGCGGAGGCTGGCGCGTGGCGCTTCTGAG 844
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluAla 300
Db 845 GAGGCGCCCGGAARAAAATAATCTTATTCATTCATTCATTCATTCATTCATTCATTC 904
QY 301 GluGluGlySer 304
Db 905 GAGGAAGCTCA 916

RESULT 10
COS79387 971 bp mRNA linear EST 20-JUL-2004
LOCUS ILUMIGEN_MCO_50239 Katze_MuLi Macaca mulatta cDNA clone
DEFINITION ILUMIGEN_17608 5' similar to Bases 6 to 971 highly similar to human
CA9 (Hs.63287), mRNA sequence.
ACCESSION COS79387
VERSION COS79387.1 GI:50410317
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecoidea; Macaca.
REFERENCE 1 (bases 1 to 971)
AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.15. 725 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:

illumigen Biosciences Inc. For further information, see
<http://www.macaque.org>
 PCR Primers
 FORWARD: CCCTCACTAAAGGAAACAAA
 BACKWARD: CACTATAGGCGCAATTGGTA
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 Seq primer: CCCTCACTAAAGGAAACAAA
 POLYA=No.

FEATURES

location/Qualifiers
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 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBIUM:17608"
 /sex="male"
 /dev_stage="adult"
 /lab_host="Electromax DH10B"
 /clone_lib="Katze WML"
 /note="Organ: ileum; Vector: pDONR 222; Site 1: Berg I;
 Site 2: Berg I; Created from Cloneminer cDNA Library
 Construction kit (catalog #18249-029)"

ORIGIN

Alignment Scores:

Pred. No.:	3e-107	Length:	971
Score:	1452.50	Matches:	286
Percent Similarity:	88.92%	Conservative:	11
Best Local Similarity:	85.63%	Mismatches:	20
Query Match:	59.92%	Indels:	17
DB:	7	Gaps:	2

US-09-967-237A-2 (1-459) x COS79387 (1-971)

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QY 55 G|YGLuAspAspProLeuG|YGLuAspLeuProSeG|LuG|uAspSerProArgG|u 74
Db 3 GGGGAAGATGACCCACATGATGAGAGGATCTGCCAGTAAAGATCCACAGAGAG 62
QY 75 G|uAspProProG|YGLuG|uAspLeuProG|YGLuG|uAspLeuProG|YGLuG|uAsp 94
Db 63 GAGAGTCA-----CCAGAGAGAGAT 86
QY 95 LeuProG|uVal|ysPro|ysSerG|uG|uG|Yser|u|ysLeuG|uAspLeuPro 114
Db 87 CTACCTGAAGTAAAGCTTAATCAGAAAGAGAGGCTCCCTGAAGTAAAGATCTA 146
QY 115 ThrValG|uAla|aProG|YAspProG|uG|uProG|uAspAsn|a|H|saGAsp|yG|u 134
Db 147 ACTGTTGAGGCTCTGAGATCTCAAGAACCCAGATATATGCCACAGGACAAAGAA 206
QY 135 G|YAspAsp|InserH|sTPA|gTYG|Y|AspPro|Trp|Pro|ArgVal|SerPro 154
Db 207 GGGGATTAACAGAGACACTGGCCCTATGAGGAGACCCGCCCTGCCCAAGGTCTCCCA 266
QY 155 AlaCysAlaG|YArgPheG|InserProVal|Asp|Lea|rgProG|uLeuAla|aPheCys 174
Db 267 GCCTGGCGGGCGCTTCCAGTCCCGGTAGATATCCGCCCAAGCTCGCGCTTCTGC 326
QY 175 ProAlaLeuArgProLeuG|uLeuLeuG|YPheG|uLeuProProLeuProG|uLeuArg 194
Db 327 CCGGCCCTGGAGCCCTGGAACTCTGGGCTTGAGCTCCGCTGCCCAAGCTGGCG 386
QY 195 LeuArgAsnAsnG|YH|sSerVal|G|uLeuThrLeuProProG|YLeuG|uMetAla|u 214
Db 387 CTCGCGACAAATGCGCACTGTGCAACTGACCTTCCGGGCTAGAGATGCTCTG 446
QY 215 G|YProG|YArgG|uYArgAla|eug|uLeuH|s|eunH|s|TrpG|YAla|aG|YArg 234
Db 447 GGTCCCGGGGAGATACCGGCTCTGACATCTGACATGCGGGGTGCTGTAGGTCGT 506
QY 235 ProG|YSerG|uH|s|ThrVal|G|uG|YH|sArgPheProAla|G|u|LeH|sVal|ValH|s 254

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Db 507 CCGGGCTCGAGACACTGTGAGAGCCAGCTTCTCCCTGCCAGATCCAGTGTTCAC 566
QY 255 LeuSerThrAlaPheAlaArgVala|aP|uAla|eug|YArg-ProG|Y|YLeuAlaVa 274
Db 567 ATACGACACCCCTATATGCAAGTGAAGAGCCTTGGGGGCCCCCGGAGCCTTGCGCT 626
QY 274 |LeuAla|aPheLeuG|uG|uG|YProG|uG|uAsnSerAla|Y|YG|uG|uLeuLeuSe 294
Db 627 GTTGGCCGCTTCTGAGAGAGGCGCGGAAACAGTGCCTATGAGCAGTGTGCTGTC 686
QY 294 rArgLeuG|uG|uAla|G|uG|uG|YserG|uTrpG|uValProG|YLeuAsp|LeSe 314
Db 687 TCACCTGGAAGAAATGCTGAGAGAGCTCAGACACTCAGCTCCAGAGCTGACGTATC 746
QY 314 rAlaLeuLeuProSerAspPheSerArg|Y|PheG|InTYG|uG|YserLeuThrTrp 334
Db 747 TGCACTCCGCTCCCTGACCTCAGCCGCTACTTCGATATGAGGGGTCTGACTACAG 806
QY 334 oProCyAlaG|uG|YVal|LeTrp-ThrValPheAsnG|uTrValMetLeuSerAla 354
Db 807 GCCCTGGCCAGGGGTGTCTGAGGACTGTGTTTACAGACAGATGCTGAGTCTA 866
QY 354 yseG|uLeuH|s|ThrLeuSerAspThrLeu-TrpG|YProG|YAspSer-ArgLeuG|uLe 373
Db 867 ACCACCTCCACCCCTCTCTGAAGCCCTGGGGGAGCTGGGAGCTCTCCGCTTACGGCT 926
QY 373 uAspHe---ArgAlaThrG|uProLeuAsnG|Y 383
Db 927 GAACCTTCGAAAGGAGACCCACCTTGGAATGG 960

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RESULT 11
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 LOCUS
 DEFINITION
 AL55184 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DK007YK10 5-PRIME, mRNA sequence.
 AL55184
 VERSION
 AL55184.3 GI:45859924
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 927)
 AUTHORS
 Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
 TITLE
 Full-length cDNA libraries and normalization
 JOURNAL
 Unpublished (2001)
 COMMENT
 On Feb 15, 2001 this sequence version replaced gi:31276993.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5300.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DK007BF05QPlc=5300.f>.

FEATURES

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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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 /cell_type="HELA CELLS COT 25-NORMALIZED"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Db 773 CTTGCCGAGATCCAGTGTTCACCTTCAGACCGCCTTTCCAGAGTTGACGAGGCTTTG 714
Qy 267 GtYArProglYglYleuAlaValAlaPheleugluGlYProgluGlYAsn 286
Db 713 GGGCGCCCGGAGGCGCTGCTGTTGGCCGCTTTCTGAGAGAGGCGCGGAAGAAAC 654
Qy 287 SerAlaTyrgluGlYleuLeuSerArYgluGlYlIleAlaGlYglYSerGlYThr 306
Db 653 AGTGCCTATGACAGTGGCTSTCTCCGCTTGAAAGMAATCCCTGAGAGAGGCTCAGAGACT 594
Qy 307 GlYValProglYleu--AspIleSerAlaIleuLeu-ProSerAspPheSerArg-TyrPh 325
Db 593 CAGGTCCAGACACTCGGACATCTCTGACCTCTCGCCCTCTCACTTCAGCCGCCACTT 534
Qy 325 eglYTyrgluGlYSerleuThrThrProProCySAAlaGlYlIleTrrThrValPh 345
Db 533 CCATATGAGGGGTCTCTGACTACACCGCCCTGTGGCCAGAGTGTACTGTGACTGTGT 474
Qy 345 eAeNgInThrValMetleuSerAlaYsgInLeuHsThrLeuSerAspThrLeuTrpGl 365
Db 473 TAAACAGACAGTATGCTGAGTCTAAGCAGCTCCACACCTCTCTGACACCTGTGGGG 414
Qy 365 YProglYAspSerArYgluGlYleuLeuPheArYAlaThrGlYProleuSnglYArYVa 385
Db 413 ACCTGTACTCTCGGCTACAGCTGAACCTCCGAGCAGCAGCCTTGTGATGGGAGGT 354
Qy 385 lIleGlYAlaSerPheProAlaGlYValAAspSerSerProArYAlaAlaGlYProValGl 405
Db 353 GATTGAGGCTCTCTCTGCTGAGTGCACAGACAGTCTCTGGGCTGTCTAGCAGTCCA 294
Qy 405 nLeuAsnSerCyaleuAlaAlaGlYAspIleleuAlaIleuValPheGlYleuLeuPheAl 425
Db 293 GCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234
Qy 425 aValThrSerValAlaPheleuValGlYMetArYArgGlnHsArYArgGlYThrYsgl 445
Db 233 TGTCCACAGGCTGCTGCTTCTGTGACATGATGAGAGCAGACAGAGGGAACCAAGG 174
Qy 445 YglYValSerTyArYProAlaGlYValAlaGlYThrGlYAla 459
Db 173 GGGTGTGAGCTACCGCCACAGAGGTAGCCGAACCTGAGAGCA 131
RESULT 13
Bg386425 874 bp mRNA linear EST 12-MAR-2001
Bg386425 60245652F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:458369 5',
LOCUS mRNA sequence.
DEFINITION Bg386425
ACCESSION Bg386425
VERSION Bg386425.1 GI:13279871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 874)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rgsabers-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCMI308 row: h column: 14
High quality sequence stop: 714.
location/Qualifiers
1..874
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:458369"
/issue="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_15"
/note="Organ: colon; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACTGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
ORIGIN
Alignment Scores:
Pred. No.: 2 5e-95 Length: 874
Score: 1304.50 Matches: 266
Percent Similarity: 92.15% Conservative: 4
Best Local Similarity: 90.78% Mismatches: 14
Query Match: 53.82% Indels: 11
DB: Gaps: 2
US-09-967-237a-2 (1-459) x Bg386425 (1-874)
Qy 66 ProSerGlYglYAspSerProArYglYAspProglYglYlIleuAspLeuProglY 85
Db 2 CCCAGTGAAGAGGATTCACCCAGAGAGAGAGATCCACCGAGAGAGATCTACCTGGA 61
Qy 86 GlYglYAspLeuProglYglYglYAspLeuProglYValIleYAspSerGlYglYlIle 105
Db 62 GAGGAGAGTCTTACTGAGAGAGAGATCTTACCTGAAGTTAAGCTTAATCAGAAAGAG 121
Qy 106 GlYSerleuYleuGlYAspLeuProTrValGlYAlaProglYAspProglYlIlePro 125
Db 122 GGTCTCTGAAAGTTAAGAGATCTTACTTGAAGCTTCTGAGATCTCTCAAGAACCC 181
Qy 126 GlYAsnAsnAlaHsArYAspYsglYlIleAspAspGlnSerHsTrpArYglYglY 145
Db 182 CAGATTAATGCCACAGAGGACAAAGAGGAGATGACAGATATGTCGCTATGAGAGGC 241
Qy 146 AspProProTrProArYValSerProAlaCyAlaGlYArPheGlnSerProValAsp 165
Db 242 GACCGCCCTGCGCGCGGCTGCTCCAGCTGCGCGCGGCTTCCAGTCCCGGTGGAT 301
Qy 166 lIleArYProglYleuAlaAlaPheCySProAlaIleuArYProleuGlYleuGlYlIle 185
Db 302 ATCCGCGCCAGTCTGCGCTTCTGCTGCGCGCTGCGCGCTGGAATCTCTGGGCTTC 361
Qy 186 GlYleuProProleuProglYleuArYglYAspAsnGlnYHsSerValGlYleuThr 205
Db 362 CAGCTCCGCGCGCTCCAGAACTGCGCGCTGCGCAATGCGCAAGTGTCAACTGACC 421
Qy 206 leuProProglYleuGlYleuAlaIleuGlYProglYArYglYlIleuGlYlIleuGlY 225
Db 422 CTGCTCTCTGAGTAAAGATGCTGTGGGCTCCGGCGGAGAGTACCGGGCTCTGCAAGCTG 481
Qy 226 HsleuHsTrpGlYAlaAlaPheArYProglYSerGlYHsTrpValGlYglYHsArY 245
Db 482 CATCTGACATCGGGGGCTGCAAGTCTCTCGGGCTGGACACACTTGGAGAGCCACCGT 541
Qy 246 PheProAlaGlYlIleHsValAlaHsleuSerThrAlaPheAlaArYValAspGlYAla 265
Db 542 TTCCCTCGGAGATTCACAGTGTTCACCTCAGACACCGCTTTGCGAGTTCGAGGGCC 601
Qy 266 leuGlYArYProglYglYleuAlaValIleuAlaAlaPheleuGlYglYProglYlIle 285
Db 602 TTGGGGCGCGGAGATGTGAGCTGTGGCCGCTTCTGGAGGA-GGGCGGAGAGAC 660
Qy 286 AsnSerAlaTyrgluGlYleuLeuSerArYglYglYlIleAlaGlYglYSerGlY 305
Db 661 AACAGTCTTATGAGAGTGTCTCTCCGCTGGAAGAAATCCCTGAGAGAGGCTCAGAG 720

Qy 306 Thr-GlnValPro-GlyLeuAspIleSerAlaLeu-----ProSerAspPheS 322
Db 721 AATCAGAGGCCCAAGACTGACATT-----ATCTTGATCTTGACTTCTGACTTCA 774
Qy 322 eRaGTYr-PheGlnTYrGluGlySer-LeuThrThProProCyAlaGlnGlyVal11 341
Db 775 AGCGTACTTTCATATGAGGAGGCGGCGGAAATACACCGGCTGTGACAGGGGTGTAC 834
Qy 341 eTrpThrValPheAsnGlnThrValMetLeu 351
Db 835 CGG-AGTGTGTATTACCCAGACATGATGCTT 864

RESULT 14
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BX383092 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DU005YG10 5-PRIME, mRNA sequence.
ACCESSION BX383092
VERSION BX383092.2 GI:46573530
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 836)
AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30449113.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnas/CS0DU005BD05QPL&c=5300.f.
Location/Qualifiers
1. 836
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DU005YG10"
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/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 8,73e-88 Length: 836
Score: 1211.00 Matches: 247
Percent Similarity: 88.57% Conserves: 1
Best Local Similarity: 88.21% Mismatches: 19
Query Match: 49.96% Indels: 16
DB: 5 Gaps: 4

US-09-967-237a-2 (1-459) x BX383092 (1-836)

Qy 1 MetaAlaProLeuCySPosePProTPrProLeuLeuIleProAlaProAlaProGly 20
Db 40 ATGGCTCTCCCTGTSCCCAAGCCCTGGCTCTCTGTTGATCCCGGCCCTGCTCCAGGC 99
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40

Db 100 CTCACGTGCAACTGCTGCTGTCTCACTGCTGCTTGTGATGCTGTCATCCACAGAGTTG 159
Qy 41 ProArgMetGlnGluuAspSerProLeuGlyGlyGlySerGlyGlyuAspAspProLeu 60
Db 160 CCCCGAATGCAAGAGATCTCCCTTGGAGAGAGCTCTTGGAGAGAGATCCACTG 219
Qy 61 G1GlyGluGluAspLeuProSerGlnGluuAspSerProArgGlnGluuAspProGlyGly 80
Db 220 GCGCAGAGAGATCTGCCAATGAGAGATTCACCCAGAGAGAGATCCACCCGAGAG 279
Qy 81 GluAspLeuProGlyGluGluuAspLeuProGlyGlyGluuAspLeuProGlyValIAspPro 100
Db 280 GAGGATCTACCTGAGAGAGATCTACCTGAGAGAGATCTACCTGAAGTTAAAGCT 339
Qy 101 LysSerGlnGluGluGlySerLeuLeuGluuAspLeuProTPrValGluuAspProGly 120
Db 340 AAATCAAGAGAGAGGCTCCGAAATGTGAGAGATCTACTGTTGAGGCTCTGGA 399
Qy 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 400 GATCTCAAGAACCCCAAGATTAATGCCACAGAGCAAAAGAA----- 441
Qy 141 TrpArgTYrGlyGlyAspProProTPrProArgValSerProAlaCyAlaGlyArgPhe 160
Db 442 -----GGCAGCCGCGCTGGCCCGGGGTGTCCAGCGCTGCGCGCGCTTC 489
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCySPProAlaLeuArgProLeu 180
Db 490 CAGTCCCGGAGATATCCCGCCCACTGCGCGCTTGTGCGCGCGCTGCGCGCGCTG 549
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlyLeuArgLysArgAsnGlyHis 200
Db 550 GAATCTTGAGGCTTCCAGCTCCGCCCTCCAGAACTGCCCTGCGCAATAGGSCAC 609
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetaAlaLeuGlyProGlyArgGlyTr 220
Db 610 AGTGTCAACTGACCTGCTGCTGCTGAGATGAGTGTGCTGCGGCTCCGCGCGAGATAC 669
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlyHisThr 240
Db 670 CGGCTCTGAGCTGACATCTGACATGGGGGAGGTGACAGTGTGCTGCGCTGCCR-SMMACT 728
Qy 241 ValGlnGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Db 729 GTGAAAGCCACs--TTTCTTCCGAAATCMC-GTGTTCACCCACACACGCTTTC--- 782
Qy 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 783 CAAGTTGAGAGAGCTTGGGS---CCCGAGRGCTGSGC--KKTTCGCGCTTGTGGAG 836

RESULT 15
CK971835 740 bp mRNA linear EST 16-MAR-2004
LOCUS 4088027 BARC 980V Bos taurus cDNA clone 980VA_M12 5', mRNA
DEFINITION sequence.
ACCESSION CK971835.1 GI:45489809
VERSION CK971835
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 740)
AUTHORS Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
G.P., Bosaik, S., Rubenfield, M. and Gasbarre, L.C.
TITLE Production of EST from cDNA libraries derived from immunologically
activated bovine gut
JOURNAL Unpublished (2004)
COMMENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA

Tel: 3015048416
Fax: 3015048414
Email: cadsanri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alc " -trim.fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 18
Plate: 4 row: M column: 12
Seq primer: CCCAGTCACGACGCTGTMAACG
High quality sequence stop: 740.
Location/Qualifiers

FEATURES
source

1..740
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV4_M12"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_11b="BARC 9BOV"
/note="Organ: Abomasum; Vector: pAGEN-1; Site 1: EcorV;
Site 2: NotI; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Osterlaga osterlagi was initiated at 15 weeks
of age. fundic and pyloric abomasum"

ORIGIN

Alignment Scores:

Pred. No.:	2,67e-81	Length:	740
Score:	1130.00	Matches:	213
Percent Similarity:	92.28%	Conservative:	14
Best Local Similarity:	86.59%	Mismatches:	19
Query Match:	46.62%	Indels:	0
DB:	7	Gaps:	0

US-09-967-237A-2 (1-459) x CK971835 (1-740)

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Db 1 CGCCCGGAGCTCACTGGTTTGTTCAGCCCTGGGCCCTGGAAATTCCTTGCGTTTGAG 60
QY 187 LeuProBleuProGlnLeuArgLeuArgAsnAsnGlyHisSerValGlnLeuThrLeu 206
Db 61 CTCGCCGCAACAACAACTGCCCTGTGCAACAACGCCACACCGGTGACGTGAGCTG 120
QY 207 ProProGlyLeuGlnuWeAlaLeuGlyProGlyArgGlnuTrArgAlaLeuGlnLeuHis 226
Db 121 CCTTCCGGGCTGAAGATGGCTTGGGTCCTCGGCGAGGATACCGGGCCCTGCAATTACAT 180
QY 227 LeuHisTrpGlyAlaAlaGlyArgProGlySerGlnuHisThrValGlnGlyHisArgPhe 246
Db 181 TTGCACCTGGGGGGCCGGGGTCCGCCGGGCTCGGAACACACGGTTGATGTCAACCGTTT 240
QY 247 ProAlaGlnuLeuHisValHisLeuSerThrAlaPheAlaArgValAspGlnuAlaLeu 266
Db 241 CTCGCCGAGATTCACTGGTTCACTCAGCACTGCATTGAGGAATTTGACGAGGCTTTG 300
QY 267 GlyArgProGlyLeuAlaValHisLeuAlaAlaPheLeuGlnuGlnGlyProGlnuGlnAsn 286
Db 301 GGGGGCCCAAGGGGCTTGGCGCTTGGCGCTTGGCGCTTGGCGAGGAGGAGGAGGAGGAG 360
QY 287 SerAlaTyrglnuLeuLeuSerArgLeuGlnuGlnuLeuAlaGlnuGlnuGlySerGlnuThr 306
Db 361 AGTGCCTATGAACAGTTGCTGTCACTTTGGAGAAATCAACGAGAAAGACTCTGAGACT 420
QY 307 GlnValProGlyLeuAspLleSerAlaLeuLeuProSerAspPheSerArgGlyrPheGln 326
Db 421 TGGGTCCCAAGACTGTGATGATCTGCACTGTGCTGCTGCACTGAGCCGCTACTTCGA 480
QY 327 TyrGlnuGlySerLeuThrThrProProCysAlaGlnuGlyValLleTrpThrValPheAsn 346
Db 481 TATGAGGGGTCTCTCACACACACCCCTGTGCGCAGGGGGTCACTGTGACTGTGTTCAAC 540
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QY 347 GlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSerAspThrLeuTrpGlyPro 366
Db 541 CAGACAGTGAAGCTGAGTGTAGACAGCTCCACACCCCTCTGACTCCCTGTGGGAGCT 600
QY 367 GlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnProLeuAsnGlyValLle 386
Db 601 GATGACTCTCGGCTGAGCTGAACCTCCGAGCTACGACGCTTTGAATGGCGAATTAAT 660
QY 387 GlnAlaSerPheProAlaGlyValAspSerProArgAlaAlaGlnuProValGlnLeu 406
Db 661 GAGGCTCTCTTCCCGCTGCGCTGAGATGGCAGGCCCTTAGACTGTGAACAGTCCCACTG 720
QY 407 AsnSerCysLeuAlaAla 412
Db 721 AATTCCGTCTCGCTGCT 738
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Search completed: August 20, 2005, 01:25:18
Job time : 4572 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: August 19, 2005, 22:15:59 ; Search time 887 Seconds

(without alignments)
3361.991 Million cell updates/sec

Title: US-09-967-237A-2

Perfect score: 2424
Sequence: 1 MAPICPSPWMLIPAPARG.....RRGTGGSYRPAEATENGA 459

Scoring table:

BLOSUM62		
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Ygapop 10.0 ,	Ygapext 0.5	
Fgapop 6.0 ,	Fgapext 7.0	
Delop 6.0 ,	Delext 7.0	

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO.epool/US09967237/runat_18082005_102620_140/app_query.fasta_1.647
-DB=Published Applications NA -PFMT=fastcap -SUFFIX=p2n.rmpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blousum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=ppc -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09967237@cgn_1_1480@runat_18082005_102620_140
-NCPU=6 -ICPU=3 -NO WMAP -LARGEOUTERY -NEG SCORES=0 -WAIT -DSPILOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications NA:*

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; Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2424	100.0	1519	15 US-10-102-524-1695	Sequence 1695, Ap
2	2424	100.0	1522	9 US-09-772-719-1	Sequence 1, Appli
3	2424	100.0	1522	10 US-09-967-237-1	Sequence 1, Appli
4	2424	100.0	1522	20 US-10-795-933-5	Sequence 5, Appli
5	2424	100.0	1522	21 US-10-888-694-1	Sequence 1, Appli
6	2424	100.0	1522	21 US-10-921-590-1	Sequence 1, Appli
7	2424	100.0	1522	22 US-10-723-795-1	Sequence 89, Appli
8	2424	100.0	1552	9 US-09-954-466-89	Sequence 726, App
9	2424	100.0	1552	9 US-09-954-466-726	Sequence 1080, Ap
10	2424	100.0	1552	10 US-09-960-706-1080	Sequence 516, App
11	2424	100.0	1552	10 US-09-873-367C-516	Sequence 213, App
12	2424	100.0	1552	11 US-09-968-007A-213	Sequence 11, Appli
13	2424	100.0	1552	15 US-10-301-822-11	Sequence 9, Appli
14	2424	100.0	1552	17 US-10-465-572-9	Sequence 574, App
15	2424	100.0	1552	17 US-10-172-118-574	Sequence 305, App
16	2424	100.0	1552	17 US-10-388-360-291	Sequence 1022, App
17	2424	100.0	1552	17 US-10-295-027-305	Sequence 574, App
18	2424	100.0	1552	17 US-10-295-027-1022	Sequence 71, Appli
19	2424	100.0	1552	18 US-10-342-887-574	Sequence 460, App
20	2424	100.0	1552	19 US-10-734-564-71	Sequence 70, Appli
21	2424	100.0	1552	20 US-10-723-660-460	Sequence 94, Appli
22	2424	100.0	1552	21 US-10-921-590-70	Sequence 516, App
23	2424	100.0	1552	21 US-10-848-755A-94	Sequence 3753, Ap
24	2424	100.0	1552	21 US-10-843-614A-516	Sequence 6853, Ap
25	2424	100.0	1552	21 US-10-843-614A-3753	Sequence 295, App
26	2424	100.0	1552	21 US-10-843-614A-663	Sequence 5135, Ap
27	2424	100.0	1552	21 US-10-794-514A-295	Sequence 14, Appli
28	2424	100.0	1552	20 US-10-723-660-5135	Sequence 23, Appli
29	2424	100.0	1658	20 US-10-794-514A-321	Sequence 1, Appli
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31	2416	99.7	1572	21 US-10-938-061-14	Sequence 79, Appli
32	2416	99.7	1572	21 US-10-938-061-14	Sequence 14, Appli
33	2233	92.1	5052	20 US-10-795-933-3	Sequence 23, Appli
34	2227	91.9	1399	20 US-10-795-933-1	Sequence 1, Appli
35	2058	84.9	1248	21 US-10-794-514A-321	Sequence 321, App
36	1938	80.0	1215	21 US-10-794-514A-323	Sequence 321, App
37	1596	65.8	1865	21 US-10-921-590-79	Sequence 79, Appli
38	1176.5	48.5	10898	9 US-09-772-719-5	Sequence 5, Appli
39	1176.5	48.5	10898	10 US-09-967-237-5	Sequence 5, Appli
40	1176.5	48.5	10898	21 US-10-888-694-1	Sequence 3, Appli
41	1176.5	48.5	10898	21 US-10-921-590-3	Sequence 3, Appli
42	1176.5	48.5	10898	22 US-10-723-795-3	Sequence 73, Appli
43	988	40.8	586	21 US-10-921-590-73	Sequence 28, Appli
44	714	29.5	415	9 US-09-772-719-28	Sequence 28, Appli
45	714	29.5	445	10 US-09-967-237-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1
US-10-102-524-1695
; Sequence 1695, Application US/10102524
; Publication No. US20030109434A1
GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863

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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1695
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-1695

Alignment Scores:
Pred. No.:      9,71e-228      Length:      1519
Score:          2424.00      Matches:      459
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             15           Gaps:        0

US-09-967-237A-2 (1-459) X US-10-102-524-1695 (1-1519)

QY      1  MecalAProLeuCysProSerProTIPLeuProLeuLeuIleProAlaProAlaProGly 20
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QY      21  LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHISProGlnArgLeu 40
DB      70  CTCACCTGTGCACTGCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129
QY      41  ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB      130  CCCCAGATGAGAGAGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAAATGATCCACTG 189
QY      61  GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
DB      190  GGGCAGAGAGATTCGCCAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 249
QY      81  GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyValIlePro 100
DB      250  GAGGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCTGAAATTAACTCT 309
QY      101  LysSerGlnGlnGlnGlySerLeuLeuLeuGluAspLeuProThrValGlnAlaProGly 120
DB      310  AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACCTGTTGAGGCTCTGGA 369
QY      121  AspProGlnGluProGlnAspAsnAlaHISArgAspLysGlnGluAspAspGlnSerHis 140
DB      370  GATTCCTAAGAAACCCAGAAATAAATGCCACAGGAGAGAGAGATTCACAGATCAT 429
QY      141  TrpArgTyrGlyGlyAspProProTIPProArgValSerProAlaCysAlaGlyArgPhe 160
DB      430  TGGCGCTATGAGAGCGACCCGCCCTGGCCCGCGGTGTCCAGGCTGTCCGCGCGCTTC 489
QY      161  GlnSerProValAspLleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB      490  CAGTCCCCGGTGTATTCGCCGCCACAGCTGCGCTTGTGCGCGCGCTGCGCGCCCTG 549
QY      181  GlnLeuLeuGlnPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlyHis 200
DB      550  GAACTCTGTGGGCTTCCAGCTCCGCCCTCCCAACATGCGCCGCCCAACAAGGCGCAC 609
QY      201  SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyTyr 220
DB      610  AGTGTGCACTGACCTGCTGCTGCGGTAGAGATGCTGCTGCGGTCCCGGGCGGAGTAC 669
QY      221  ArgAlaLeuGlnLeuHISLeuHISerTrpGlyAlaAlaGlyArgProGlySerGlnHISThr 240
DB      670  CGGGCTCTGAGCTGCACTGCACTGGGGGCTGCAAGTGTGCTGCGGCTCGAGACACT 729
QY      241  ValGlnGlyHISArgPheProAlaGlnIleHISValValHISLeuSerTrpAlaPheAla 260
DB      730  GTGGAAAGCCACCGTTTCCCTGCGAGATTCACCTGTGTTCACCTCCACACCGCTTTGGC 789
QY      261  ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
DB      790  AGAGTTACAGAGGCTTGGGGCGCGCGGAGGCTGTGCGGTGTGCGCGCTTTCTGGAG 849
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QY      281  GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
DB      850  GAGGCGCCGAGAAACAGTGCCTATGACAGATGCTGTCTGCTGGAAGAAATGCTCT 909
QY      301  GlnGlnGlySerGlnThrGlnValProGlyLeuAspLleSerAlaLeuLeuProSerAsp 320
DB      910  GAGAAAGCTCAGAGATCAGGTCCTCCAGAGACTGACATATCTGACTCTGCGCTTGAC 969
QY      321  PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
DB      970  TTACAGCGGCTACTTCCATATGAGGGCTCTCTGACTACACCGCCCTGCGCGGGTGC 1029
QY      341  IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHISThrLeuSer 360
DB      1030  ATCTGACTGTGTTTAAACAGACAGATGATCTGATGCTTAAGCAGCTCCACACCTCTCT 1089
QY      361  AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnMetArgAlaTrnGlnPro 380
DB      1090  GACACCTGTGGGAGACTGTGACTCTGCGCTACGCTGAATTCGAGGAGAGAGAGCTCT 1149
QY      381  LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB      1150  TTGAATGGGAGAGATGAGGCTCTCTCTGCTGAGTGAACAGCACTCTCGGGCT 1209
QY      401  AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLleLeuAlaLeuValPhe 420
DB      1210  GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1269
QY      421  GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHISArg 440
DB      1270  GGCTCTCTTTTGTGTGACAGAGGTGCGTCTCTTGTGAGATGAGAAAGGAGACAGAGA 1329
QY      441  ArgGlyThrLysGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
DB      1330  AGGGGAACCAAGGGGTGTGACTACCGGCCAGAGAGGTTAGCCAGACTGGAGGCC 1386

RESULT 2
US-09-772-719-1
; Sequence 1, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
```

TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-772-719-1

Alignment Scores:

Pred. No.:	9,746-228	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-967-237a-2 (1-459) x US-09-772-719-1 (1-1522)

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QY      1 MetAlaProLeuCyseProSerProTrrpLeuProLeuLeuIleProAlaProAlaProGly 20
DB      13 ATGGCTCCCTGTCGCCCCAGCCCTGGCTCCCTGTTGATCCCGGCCCTGCTCCAGAGC 72
QY      21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB      73 CTCACGTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
QY      41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB      133 CCCCGGATCCAGAGAGATTCCTCCCTTGGAGAGAGCTCTTGGGGAGATACCCACTG 192
QY      61 GlyGluAspLeuProSerGlyGluAspSerProArgGlyGluAspProProGlyGlu 80
DB      193 GGCAGAGAGATCTGCCAGATGAAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 252
QY      81 GluAspLeuProGlyGlyGluAspLeuProGlyGlyGluAspLeuProGlyValLeuPro 100
DB      253 GAGGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCTGAAAGTTAAGCTT 312
QY      101 LysSerGlnGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGlnAlaProGly 120
DB      313 AATATGAGAGAGAGAGAGCTCCCTGAAATTAGAGATCTACCTGCTTGAAGCTCTGGA 372
QY      121 AspProGlnGluProGlnAsnAsnAlaHisArgAspGlyGlyGluAspAspGlnSerHis 140
DB      373 GATCCTCAAGAAACCCAGAAATATATCCCAAGAGGCAAAAGAGGATGACCAAGATCAT 432
QY      141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
DB      433 TGGCCCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
QY      161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB      493 CAGTCCCGGCTGAGATATCCGCCCAAGCTCCGCCCTTCTGCGGAGCCCTGCGGCCCTG 552
QY      181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlyHis 200
DB      553 GAACTCTGGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTCGCAACAATGGCCAC 612
QY      201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlnTyr 220
DB      613 AGTGTCAACTGACCTCTCTCTGAGGCTAGAGAGAGCTCTGAGGCTCCGGGGGAGAGTAC 672
QY      221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlyHisTrp 240
DB      673 CGGGCTCTGCAAGCTGCACTGAGCTGGGGGCTGAGAGTCTGCGGGCTCGAGACACT 732
QY      241 ValGlyGlyHisArgPheProAlaGluIleHisValAlaHisLeuSerThrAlaPheAla 260
DB      733 GTGGAAGGCCAACCGTTTCCCTGCGCAGAGATCCAGTGTTCACCTCAGACACCGCTTTGCC 792
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QY      261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValAlaLeuAlaPheLeuGlu 280
DB      793 AGAGTTGACGAGAGCTTTGGGGGCCCCGGAGAGCTTGGCCGCTTTTGTGAG 852
QY      281 GlnGlyProGlnGluAsnSerAlaTyrGlnLeuLeuSerArgLeuGlnGluIleAla 300
DB      853 GAGGGCCCCGGAAGAAAACAGTGCCATGAGCAGATTGCTGCTCGCTTGAAGAAATCCCT 912
QY      301 GlyGlyGlySerGlyThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
DB      913 GAGGAAGGCTCAGACACTCAGGTCCAGAGACTGACATATCTGCACTTCCCTCCCTAC 972
QY      321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrTrpProProCysAlaGlnGlyVal 340
DB      973 TTCACCCCTCTCTTCAATATGAGGAGCTCTGACTTACACCGCCCTGAGCCAGGATGC 1032
QY      341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaTyrGlnLeuHisThrLeuSer 360
DB      1033 ATCTGCACTGTGTTTAAACAGACAGTGAATGCTGAGTGTCTAAGCAGCTCCACACCTCTCT 1092
QY      361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
DB      1093 GACACCTCTGTGGGAGCTGTGACTCTCGCTACAGCTGAACCTTCCGAGCAGCAGAGCT 1152
QY      381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB      1153 TTGAATGGCCAGAGATTAAGAGCTCTCTTCCCTGCTGAGAGTGAAGACAGAGATCTCGGCT 1212
QY      401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
DB      1213 GCTGAGCAGTCCAGACTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY      421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
DB      1273 GGCCTCTCTTTTGGCTGTCACACGAGCTGCTTCTTGTGCAAGATGAGAGAGCAGACAGA 1332
QY      441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyVala 459
DB      1333 AGGGAGACCAAGGGGGTGTAGCTTACCGCCAGCAGAGGTAGCCAGACTGGAGCC 1389
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RESULT 3
US-09-967-237-1
; Sequence 1, Application US/09967237
; Publication No. US20030049826A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: NM Gene and Protein
; FILE REFERENCE: D-0021.58-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-09-967-237-1

Alignment Scores:
Pred. No.: 9,746-228 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-967-237A-2 (1-459) x US-09-967-237-1 (1-1522)

QY 1 MetAlaProLeuCySProSerProTIPLeuProLeuLeuIleProAlaProAlaProGly 20
DB 13 ATGGCTCCCTGTCGCCAGCCCTCGGCTCCCTGTTGATCCCGGCCCTCGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 73 CTACCTGTGCACTGCTGCTGTCTGCTGCTGTGATGCTGTCCATCCCAAGGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB 133 CCCGGATGAGAGAGATTCCCTTGAGAGAGGCTCTTGCGGAAGATGACCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
DB 193 GGCAGAGAGATCTGCCAGTGAAGAGATTCACTCCAGAGAGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValHisPro 100
DB 253 GAGATCTACCTGAGAGAGAGATCTACCTGAGAGAGATCTACCTGAACTTAAGCTT 312
QY 101 LysSerGluGluGluGlySerLeuLeuGluGluAspLeuProThrValGluAlaProGly 120
DB 313 AAATCAGAGAAGAGGCTCCCTGAACTTGAAGATCTTACTTACTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
DB 373 GATCTCAAGAACCCCAAGATTAAGCCACAGAGAGAAAGAGGATGACCAAGATCAT 432
QY 141 TrpArgTyrGlyGlyAspProProTIPProArgValSerProAlaCysAlaGlyArgPhe 160
DB 433 TGGGGCTATGAGAGCGACCGCCCTGGGCCCGGGGTGTCCCAAGCTCGGGGCGGCTTC 492
QY 161 GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 493 CAGTCCCGGTGATATCCGCCCCCACTGCGCCCTTGTGCCCGGCGCTGCGGCCCTG 552
QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuAlaGlnAsnArgHis 200
DB 553 GAATCTCTGGGCTTCCAGCTCCCGCCCTCCCAACTGGCGCTCCCAACAAAGGCGCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
DB 613 AGTGTGAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisSerGlyValAlaGlyArgProGlySerGluHisThr 240
DB 673 CGGGCTCTGAGCTGCACTGCACTGGGGGCTGCAAGTGGCTCGGCGCTCGAGCACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisValHisLeuSerThrAlaPheAla 260
DB 733 GTGAAAGCCACCGCTTCCCTGCGGAGATCCAGTGTTCACCTGACACCGGCTTTGGC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
DB 793 AGAGTTACAGAGGCTTGGGGCGCCCGGAGGCTGCGCTGTTGGCGGCTTTCTGAG 852
QY 281 GlyGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
DB 853 GAGGGCCCGAAGAAACAGTGCCTATGAGCAGATTGCTGCTCGCTTGAAGAAATGCT 912
QY 301 GluGlnGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
DB 913 GAGGAAGCTCAGAGACTCAGGTCCTCAGACTGAGACTGATCTGACCTCCCTTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
DB 973 TTGAGCGGCTACTTCCAAATATGAGGGGTCTGTGACTACCGCCCTGTGCGGAGGTGC 1032

QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaGlnGlnLeuHisSerLeuSer 360
DB 1033 ATCTGACTGTGTTTAACTCAGACAGTGAATGCTGATGCTTAAGCACTCCACACCTCTCT 1092
QY 361 AspThrLeuThrProGlyAspSerArgLeuGlnLeuAsnSerArgAlaThrGlnPro 380
DB 1093 GACACCTGTGGGACCTGTGTGACTCTCGGCTACAGTGAATTCAGAGGAGCGAGCTT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB 1153 TTGAATGGGAGGATGATGAGGCTCTCTTCCCTGCTGAGTGAACAGCACTCTCGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaValPhe 420
DB 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
DB 1273 GGCCTCTTTTCTGTGACACAGCGTGCCTGCTTGTGAGTGAAGAGGAGCAACA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
DB 1333 AGGGAAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTACCGAGCTGAGGCC 1389

RESULT 4
US-10-795-933-5
Sequence 5, Application US/10795933
Publication No. US20040259126A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021-2
CURRENT APPLICATION NUMBER: US/10/795,933
CURRENT FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US/08/260,190
PRIOR FILING DATE: 1994-06-15
PRIOR APPLICATION NUMBER: 08/177,093
PRIOR FILING DATE: 1993-12-30
PRIOR APPLICATION NUMBER: 07/964,589
PRIOR FILING DATE: 1992-10-21
PRIOR APPLICATION NUMBER: PV-709-92
PRIOR FILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 1522
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (13) .. (1389)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (124) .. (1389)
US-10-795-933-5

Alignment Scores:
Pred. No.: 9 74e-228 Length: 1522
Score: 2424.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0
US-09-967-237A-2 (1-459) x US-10-795-933-5 (1-1522)

QY 1 MetAlaProLeuCySProSerProTIPLeuProLeuLeuIleProAlaProAlaProGly 20
DB 13 ATGGCTCCCTGTCGCCAGCCCTCGGCTCCCTGTTGATCCCGGCCCTCGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40

Db	73	CTCAGCTGGCAACGCTGCTGCTACGCTGCTTGTATGCTGTCCATCCCGAGAGTTG	132
Qy	41	ProaHwercGlnGluAaspSerProLeuGlyGlySerSerGlyGluAaspAaspProLeu	60
Db	133	CCCCGATGACGAGAGGATTTCCCTTGAGAGAGGACTCTTCTGGGGAAAGATGACCCACTG	192
Qy	61	GlyGlyGluGluAaspLeuProSerGlnGluAaspSerProArgGlnGluAaspProGlyGlu	80
Db	193	GGCCAGAGAGGATCTGCCCCAGTGAAGAGAAATTCACCCAGAGAGGAGATTCACCCGGAG	252
Qy	81	GluAaspLeuProGlyGlnGluAaspLeuProGlyGlnGluGluAaspLeuProGlyValLeuPro	100
Db	253	GAGGATCTACCTGGAGAGAGAGATCTACCTGGAGAGAGAGATCTACCTGAAGTTAAAGCTT	312
Qy	101	LyseSerGlnGlnGlnGlySerLeuLyseGlnGluAaspLeuProThrValGlnAaprogly	120
Db	313	AAATCAGAGAGAGAGGCTCCCTGAATTGAGAGATCTACCTACTGTTGAGGCTCCCGA	372
Qy	121	AaspProGlnGluProGlnAaspAaspAhiAargAaspLyseGlnGlyAaspAaspInserHis	140
Db	373	GATCTCTAAGAACCCCAAGATTAAGCCCAAGGACAAAGAGGGATGACAGAGTCAAT	432
Qy	141	TryArgTryGlyGlyAaspProProTProArgValSerProAlaCysAlaGlyArgPhe	160
Db	433	TGGGGCTATGAGAGGACGACCGCTGGCCCGGGGTGTCCACAGCTGCGGGCCGGCTTC	492
Qy	161	GlnSerProValAaspIleArgProGlnLeuAlaAalPheCysProAlaLeuAArgProLeu	180
Db	493	CAGTCCCCGGGATATCCGCCCCACACTGGCCGCTTGGCCCGGCCCTCCGCCCTC	552
Qy	181	GlyLeuLeuGlyPheGlnLeuProProLeuProGlyLeuAargLeuArgAaspAaspGlyHis	200
Db	553	GAATCTCTGGGCTTCCAGCTCCGCCCTCCAGAACCTGGCCCTGGCCCAATATGGCCAC	612
Qy	201	SerValGlnLeuThrLeuProProGlyGlyLeuGlnMerAlaLeuGlyProGlyValArgGlyuTry	220
Db	613	AGTGTGCACTGACCCCTGCTCCCTGGGCTAGAGTGGCTGTGGGTCCCGGGCGAGGTAC	672
Qy	221	ArgAlaLeuGlnLeuHisIleuHisIleTrGlyValAalAglYArgProGlySerGlnHisIleThr	240
Db	673	CGGGCTTCGACGCTGATCTGCATCGGGGGGGCTGCAGTGTCTCGGGCTCGAGACACT	732
Qy	241	ValGlnGlyHisArgPheProAlaGlnIleHisValHisIleuSerThrAlaPheAla	260
Db	733	GTGGAAGGCCACCGTTCCTCCGCGAATCAACGTGGTCACTCAGCACCGCCCTTGGCC	792
Qy	261	ArgValAaspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAalPheLeuGlu	280
Db	793	AGAGTTACAGAGGCTTGGGGCGGCCCGAGGCGCTGGCCGTGTGGCGCGCTTTCGGAG	852
Qy	281	GlnGlyProGlnGluAaspSerAlaTryGlnGlyLeuLeuSerArgLeuGlnGlnIleAla	300
Db	853	GAGGGCCCGAAGAAAACAGTGCCTATGAGCAATGTGCTGTCTGGATGGAAATTCGCT	912
Qy	301	GlnGlnGlySerGlnThrGlnValProGlyLeuAaspIleSerAlaLeuLeuProSerAasp	320
Db	913	GAGGAAGGCTCAGAGACTCAGTCCAGACTGGAACATATCTCACTCCCTGCGCCTCGAC	972
Qy	321	PheSerArgTryPheGlnIleTryGlnGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	973	TTCAAGCCGCACTTCCAATATGAGGGGTCTCTAATAACCGGCTGTGGCCAGGGGTGTC	1032
Qy	341	IleTrpThrValPheAaspGlnThrValMetLeuSerAlaLyseGlnLeuHisIleThrLeuSer	360
Db	1033	ATCTGAGCTGTGTTAAACAGACAGATATCTAGTACTTAAGACAGCTCCACACCTCTCT	1092
Qy	361	AaspThrLeuTrpGlyProGlyAaspSerArgLeuGlnLeuAaspAaspAalArgAlaThrGlnPro	380
Db	1093	GACACCTGTGGGGAAGCTGGTGACTCTCGGCTACAGCTGAATTCGAGGGAAGGAGCTT	1152
Qy	381	LeuAaspGlyArgValIleGlnAlaSerPheProAlaGlyValAaspSerSerProAlaGlnA	400

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Db      1153  TTGAATGGGCGAGGATTGAGAGCCTCCTCTCCCTGCTGAGAGTGACAGACAGCTCCGGCT 121212
Qy      401    AlaGluProVal1GlnLeuAenSerCysLeuAlaAlaGlyAap11LeuAlaLeuValPhe 420
Db      1213  GCTGAGCCAGACGTCAGCTGAATTCTCGCTGGCTCTGGTGACATCTTAGCCCTGGTTTTT 1272
Qy      421    GlyLeuPheAlaVal1ThrSerVal1AlaPheLeuValGlnMetArgArgGlnHisArg 440
Db      1273  GGCTCTCTTTTGTGTGTGCACAGGCGTGGCTTCTTGTCAGAAAGAGAGAGGACACACAGA 1332
Qy      441    ArgGlyThrLeuSg1GlyGlyVal1SerTyrArgProAlaGluVal1AlaGluThrG1ValA 459
Db      1333  AGGGGACCAAGAGGGGCTGTGAGCTACCGCCACAGACAGTACGCCGAGACTGAGACC 1389

RESULT 5
US-10-888-694-1
; Sequence 1, Application US/10888694
; Publication No. US20050003425A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 465 California Street, Suite 450
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/888,694
FILING DATE: 08-Jul-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/772,719
FILING DATE: 30-Jan-2001
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3A-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-888-694-1

Alignment Scores:
Pred. No.: 9.74e-228 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-967-237A-2 (1-459) x US-10-888-694-1 (1-1522)

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QY 1 MetAlaProLeuCySProSerProTPrLeuProLeuLeu1LeProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTCGCCAGCCCTGGCTCCTGTTGAATCCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrAlaGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACTGTGAAACGTGCTGTCTCACTGCTGCTGTGATGCTGCTCCATCCCAAGGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGlyAspAspProLeu 60
Db 133 CCCCAGATGAGAGAGATTCCTCCCTTGGAGAGAGGCTCTTGGGGAAGATGACCACTG 192
QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGly 80
Db 193 GCGGAGAGAGATCGCCAGTGAAGAGATTCAACCAAGAGAGAGATCCACCCGAGAG 252
QY 81 GlnAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlnValLysPro 100
Db 253 GAGGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCTGAAGTTAACCT 312
QY 101 LysSerGlnGlnGlnGlySerLeuLysLeuGlnAspLeuProThrValGlnAlaProGly 120
Db 313 AAATCAGAAAGAGGCTCCTTAAGTTAGAGATCTACTGTTGAGGCTCTCGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCAAGATTATGCCCACAGGGAACAAGAGGATGACAGAGTCAT 432
QY 141 ThrArgTrpGlyGlyAspProProTPrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGGCTATGAGAGCGACCCGCTGCGCCCGGGTGTGCCAGGCTCGGGGCGCTTC 492
QY 161 GlnSerProValAspLeaArgProGlnLeuAlaIlePheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGATATCCGCCCCAGACTGCGGCTTCTGCCCGGCGCTGCGGCCCTG 552
QY 181 GlnLeuLeuGlnPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnArgLys 200
Db 553 GAATCCTGGGGCTTCCAGCTCCGCGCTCCAGAACTGGCGCTCGCAACAATGGGCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLysGlnMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTGCACTGACCTGCTCCTCGGGCTAGAGTGGCTCTGGGTCCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CGGGCTCTGAGCTGCACTGCACTGGGGGGCTGCAAGTCTCGGGCTCGAGCAACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACGCTTCCCTGCGAGATCCACGTGTTCACTCCAGACACGCGCTTGGC 792
QY 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln 280
Db 793 AGAGTTGACAGGCTTGGGGCGCGCGGAGGCTGCGCTGTTGGCGCTTTCGAG 852
QY 281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
Db 853 GAGGCGCCGGAAGAAACAGTGCCTATGACAGTGTCTGCTGCTTGGAGAAATGCT 912
QY 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGTCCAGACTGGACATATCTGCACTCGCCCTTGAC 972
QY 321 PheSerArgTrpPheGlnTrpGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTGAGCGGCTACTTCATATGAGGGGTCTCTGATCAACCGCCCTGTGCCAGGGGTTC 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisTrpLeuSer 360
Db 1033 ATCTGAGCTGTGTTTAACAGACAGTATGCTGAGTGTCAAGACGCTCCACACCTCTCT 1092

QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGGAAGCTGTGACTCTCGGCTACAGCTGAATCCGAGCGCAGGCT 1152
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerProAlaGlyAla 400
Db 1153 TTGAATGGCGAGGATGAGGCTCTCTTCCCTGCTGAGTGAACAGCACTCTCGGGCT 1212
QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLysLeuAlaLeuValPhe 420
Db 1213 GCTGAGGCACTCCAGCTGAATTCCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
QY 441 ArgGlyThrTrpGlyGlyValSerTrpArgProAlaGlnValAlaGlnThrGlyAla 459
Db 1333 AGGGAACCAAGAGGGGTGAGTACCGCCAGAGAGGTAGCCGAGACTGAGGCC 1389

RESULT 6
US-10-921-590-1
; Sequence 1, Application US/10921590
; Publication No. US20050031623A1
; GENERAL INFORMATION:
; APPLICANT: Pastorex, Jaramix
; APPLICANT: Zavada, Jan
; APPLICANT: Ortova Gut, Marta
; APPLICANT: Zlatovicova, Silvia
; APPLICANT: Pastorekova, Silvia
; TITLE OF INVENTION: SOLUBLE FORM OF CARBONIC ANHYDRASE IX (s-CA IX), ASSAYS TO DETECT
; TITLE OF INVENTION: s-CA IX, CA IX's COEXPRESSION WITH HER-2/neu/c-erbB-2 AND CA
; FILE REFERENCE: MX-2363/2376 US
; CURRENT APPLICATION NUMBER: US/10/921, 590
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: 60/358, 824
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/383, 068
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: 60/431, 499
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: PCT/US03/05136
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05137
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13) .. (1389)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (124) .. (1389)
US-10-921-590-1

Alignment Scores:
Pred. No.: 9, 74e-228 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-967-237A-2 (1-459) x US-10-921-590-1 (1-1522)

QY 1 MetAlaProLeuCySProSerProTPrLeuProLeuLeu1LeProAlaProAlaProGly 20
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Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCCCTGCTCCAGGC 72
Qy LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGCACTGCTGTGCTACGTGCTTCGATCCCTGTCATCCAGAGTTTG 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCCGATGCAAGAGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAGATACCCACCTG 192
Qy 61 GlyGluGluAspLeuProSerSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 193 GCGCAGAGAGATCTGCCCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCCGAGAG 252
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyGluPro 100
Db 253 GAGGATCTACCTGGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAACTTAAAGCT 312
Qy 101 LysSerGluGluGlySerLeuLeuGluAspLeuProThrValGluAspProGly 120
Db 313 AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACCTGTTGAGGCTCTGGA 372
Qy 121 AspProGluGluProGlnAspAsnAsnHisArgAspGlyGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAAACCCAGATATATGCCCAAGGAAAGAGGATGACCAAGATCAT 432
Qy 141 TTPATGTYTGYGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCCCTATGAGGAGGAGCCCGCCCTGGCCCGGGGTGCCCAAGCTGCGCGGCGCTTC 492
Qy 161 GlnSerProValAspAlaArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGATGATATCCGCCCAAGCTGCGCGCTTGTGCCCGCCCTGGCGCCCTCG 552
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 553 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGGCGGAACATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTCAACTGACCTGCTCTGCTGCTGAGAGATGCTGCTGGCTCCCGGAGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisIleuHisIleuHisIleuHisIleuHisIleuHisIleuHis 240
Db 673 CGGGCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValIleHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGTTCACTCAGCACCGCCTTTGGC 792
Qy 261 ArgValAspGluValLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTGAAGAGGCTTGGGCGGCCCGGAGGCGCTGGCGCTTGGCGCCCTTTCTGAG 852
Qy 281 GlyGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 853 GAGGGCCCCGAAAGAAACAGTCCCTHAGACAGTTGCTCTCGCTTGGAGAAATTCGCT 912
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAACTCAGGTCCAGGACTGAGCATATCTGCACTCCTGCTCTAC 972
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrTrpProProCysAlaGlnIleVal 340
Db 973 TTCAGCCCTACTTCAATATGAGGAGGCTCTGACTACCGCCCTGTGGCCAGGAGTGC 1032
Qy 341 IleTrpThrValPheAsnGlnThrValIleLeuSerAlaIleGlnLeuHisIleHisLeuSer 360
Db 1093 ATCTGCACTGTGTTAAACAGCACTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1092
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGCTGTGATCTCTGGCTACAGCTGAACCTTCCGAGCGACGAGCCT 1152

Qy 381 LeuAsnGlyArgValIleGluValSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGAGATATGAGGCTTCCTGCTGAGGTGAGACAGCTCTGCGGCT 1212
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGCTCAGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
Qy 421 GlyLeuLeuPheAlaValIleThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GCGCTCTTTTGTGCTGACCAAGCGCTCGCTTCTTGTGAGATGAGAAAGCAGACAGA 1332
Qy 441 ArgGlyThrIleGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAAACCAAGGGGGTGTGACTACCGCCAGCAGAGATGACCGAGACTGGAGCC 1389

RESULT 7
US-10-723-795-1
; Sequence 1, Application US/10723795
; Publication No. US20040146955A1
; GENERAL INFORMATION:
; APPLICANT: Supuran, Claudiu
; APPLICANT: Scozzafava, Andrea
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: CA IX-SPECIFIC INHIBITORS
; FILE REFERENCE: MST-2393 US
; CURRENT APPLICATION NUMBER: US/10/723,795
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,089
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 60/489,473
; PRIOR FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: 60/515,140
; PRIOR FILING DATE: 2003-10-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-10-723-795-1

Alignment Scores:
Pred. No.: 9,74e-228 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0

US-09-967-237a-2 (1-459) x US-10-723-795-1 (1-1522)

Qy 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCCCTGCTCCAGGC 72
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGCACTGCTGTGCTACGTGCTTCGATCCCTGTCATCCAGAGTTTG 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCCGATGCAAGAGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAGATACCCACCTG 192
Qy 61 GlyGluGluAspLeuProSerSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 193 GCGCAGAGAGATCTGCCCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCCGAGAG 252
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyGluPro 100
Db 253 GAGGATCTACCTGGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAACTTAAAGCT 312
Qy 101 LysSerGluGluGlySerLeuLeuGluAspLeuProThrValGluAspProGly 120
Db 313 AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACCTGTTGAGGCTCTGGA 372
Qy 121 AspProGluGluProGlnAspAsnAsnHisArgAspGlyGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAAACCCAGATATATGCCCAAGGAAAGAGGATGACCAAGATCAT 432
Qy 141 TTPATGTYTGYGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCCCTATGAGGAGGAGCCCGCCCTGGCCCGGGGTGCCCAAGCTGCGCGGCGCTTC 492
Qy 161 GlnSerProValAspAlaArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGATGATATCCGCCCAAGCTGCGCGCTTGTGCCCGCCCTGGCGCCCTCG 552
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 553 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGGCGGAACATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTCAACTGACCTGCTCTGCTGCTGAGAGATGCTGCTGGCTCCCGGAGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisIleuHisIleuHisIleuHisIleuHisIleuHisIleuHis 240
Db 673 CGGGCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValIleHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGTTCACTCAGCACCGCCTTTGGC 792
Qy 261 ArgValAspGluValLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTGAAGAGGCTTGGGCGGCCCGGAGGCGCTGGCGCTTGGCGCCCTTTCTGAG 852
Qy 281 GlyGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 853 GAGGGCCCCGAAAGAAACAGTCCCTHAGACAGTTGCTCTCGCTTGGAGAAATTCGCT 912
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAACTCAGGTCCAGGACTGAGCATATCTGCACTCCTGCTCTAC 972
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrTrpProProCysAlaGlnIleVal 340
Db 973 TTCAGCCCTACTTCAATATGAGGAGGCTCTGACTACCGCCCTGTGGCCAGGAGTGC 1032
Qy 341 IleTrpThrValPheAsnGlnThrValIleLeuSerAlaIleGlnLeuHisIleHisLeuSer 360
Db 1093 ATCTGCACTGTGTTAAACAGCACTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1092
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGCTGTGATCTCTGGCTACAGCTGAACCTTCCGAGCGACGAGCCT 1152

193 GGCAGAGGATCTGCCAGTGAAGAGATTCCACCAGAGAGGATCCACCCGGAGAG 252
Qy GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValValPro 100
Db 81 GAGGATCTAAGGAGAGAGGATCTTACCTGGAGAGGATCTTACCTGAAGTTAAGCT 312
Qy 101 LysSerGluGluGluGluSerLeuLysLeuLysLeuProThrValGluValProGly 120
Db 313 AAATCAGAGAGAGAGGCTCCCTGAGATTAGAGTCTACTACTGTTGAGGCTCTGGA 372
Qy 121 AspProGluGluProGluLysAsnAsnAlaHisArgAspLysGluGluYAspAspGlnSerHis 140
Db 373 GATCTCAAGAACCCCAAGATTAATGCCACAGAGCAAGAGGAGATGACAGAGTCAT 432
Qy 141 TTPATGT 160
Db 433 TGGGCTATGGAGGCGACCCCGCTGGCCCGGGGTGTCCAGGCTGTGGCGGCGGCTTC 492
Qy 161 GlnSerProValAspLeuArgProGluLysLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCCCAGCTCGCGCTTCTGCGCGGCTCGCGCCCTG 552
Qy 181 GluLeuLeuGluPheGlnLeuProProLeuProGluLeuAlaGluLeuArgAsnGlyHis 200
Db 553 GAATCTCTGGGCTTCAGACTCCCGCTCCAGAACTGCGCTGCGCAAAATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLysLeuLysLeuAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTGCACTGACCCCTGCTCCCTGGGTAGAGATGCTGCGGTCCCGGGCGGAGTAC 672
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTTPGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CGGCTCTGACGCTGCACTCTGCTGAGGGGCTGACGCTGCTGCGGCTCGAGACACACT 732
Qy 241 ValGluGlyHisArgPheProAlaGluLysValValHisLeuSerThrAlaPheAla 260
Db 733 GTGAGAGCCACCGTTTCCCTGCGAGATCCAGCTGTGCTCCAGACCGCTTTGGC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyLysLeuAlaValAlaAlaPheLeuGlu 280
Db 793 AGATTTACAGAGGCTTGGGGGCGCCCGGAGGCTTGGCGGCTTCTGAGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGluLeuLeuSerArgLeuGluGluAla 300
Db 853 GAGGCGCCGGAAGAAACAGTGTCTATGACAGTGTGCTGCTGCTGGAAGAAATCGCT 912
Qy 301 GlnGluGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAGGCTCAGAGACTCAGGCTCCAGAGCTGACATATGCACTTGGCCCTGAC 972
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTGACGCGCTACTTCCATATGAGGGGCTCTGACTACCGCCCTGTGGCCAGGGTGC 1032
Qy 341 LLeTTPThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1033 ATCTGCACTGTGTAAACAGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1092
Qy 361 AspThrLeuThrProGlyProGlyYAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCCCTGGGGAGCTGGGACTCTGGCTACAGCTGAACCTTCCAGACCAAGGCT 1152
Qy 381 LeuAsnGlyArgValLLeGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGGAATGGGCGAGATTTGAGGCTCTCTCTCTGAGTGTGACAGAGTCTCGGGCT 1212
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLLeuAlaLeuValPhe 420
Db 1213 GCTGAGCAGACTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440

Db 1273 GGCCTCTTTTGTCTGTACACAGCTCGCTTCTGTGTGAGATGAGAGGACACAGA 1332
Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGGAACCAAGGGGCTGTGAGTACCCGCCACAGAGGTTACCGAGACTGAGGCC 1389
RESULT 8
US-09-954-456-89
Sequence 89, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
PRIORITY FILING DATE: 2001-09-18
PRIORITY APPLICATION NUMBER: US/60/233,617
PRIORITY FILING DATE: 2000-09-18
PRIORITY APPLICATION NUMBER: US/60/234,052
PRIORITY FILING DATE: 2000-09-20
PRIORITY APPLICATION NUMBER: US/60/234,923
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,134
PRIORITY FILING DATE: 2000-09-25
PRIORITY APPLICATION NUMBER: US/60/235,637
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,638
PRIORITY FILING DATE: 2000-09-26
PRIORITY APPLICATION NUMBER: US/60/235,711
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,720
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,840
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: US/60/235,863
PRIORITY FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 89
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-89
Alignment Scores:
Pred. No.: 9,97e-228 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-967-237A-2 (1-459) x US-09-954-456-89 (1-1552)
Qy 1 MetAlaProLeuCysProSerProTTPLeuProLeuLysLeuProAlaProGly 20
Db 43 ATGGCTCCCTGTTGCCCCCAGCCCTGCTCTCTGTTGATCCCGGCCCTGTCCAGGC 102
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTACCTGTGAACTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162
Qy 41 ProArgMetGlnLysAspSerProLeuGlyGlySerSerGlyLysAspProLeu 60
Db 163 CCGCGATGACAGAGATTTCCCTTGGAGAGGCTCTTCTGGGGAAGATGACCACTG 222
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 223 GCGAGAGAGATCTGCCAGTGAAGAGATTCAACAGAGAGGATTCACCCCGGAGAG 282
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValValPro 100

283 GAGGATCTACTGAGAGAGGATCTACTGAGAGAGGATCTACTGAAATTAAAGCT 342
QY 101 LysSerGluGluGlySerLeuGluuAspLeuProThrValGluuLapProGly 120
Db 343 AAATAGAAAGAGAGGCTCTCTGAAATAGAGATCTACTGTTAGGCTCTCTGGA 402
QY 121 AspProGluGluProGluuAspAsnAlaHisArgAspGlyGlyValAspAspGlnSerHis 140
Db 403 GATCTCTAAGAACCCCAAGATATATGCTCCAGAGCAAAAGAGGATATACCAAGACTCAT 462
QY 141 TTPArgTYrGlyValAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCCCTATGAGAGGAGCCCGGCTGGCCCCGGGGTGTCCCCAGCCCTGGCGGGCGCTTC 522
QY 161 GlnSerProValAspLLeuArgProGluuAlaAlaPheCysArgProAlaLeuArgProLeu 180
Db 523 CAGTCCCGGAGTAAATCCGCCCCAGCTCGCGCCCTTCCTGCGCCGCGCCCTGGCCCCCTG 582
QY 181 GluLeuLeuGlyPheGluLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 583 GAACTCTCGGCTTCCAGCTCCCGCGCTCCAGAACTCGCTGGCAACATGCGCAC 642
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTrp 220
Db 643 AGTGTCAACTGAACTGCTGCTCTGGGCTAGAGATGCTCTGGGTCTCCGGCGGAGGTAC 702
QY 221 ArgAlaLeuGlnLeuHisGluHisStrpGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 703 CGGGCTGTGCACTCATCTGCACTGGGGGGTGTGCAAGTGTCTCGGCTCGAGACACT 762
QY 241 ValGluGlyHisArgPheProAlaGluLeuHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCTTTCCCTCCGAGATCCAGTGTTCACCTCAAGCACCCCTTTGGC 822
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTGACAGAGGCTTGGGGCGCCCGGAGGCTGTGGCTGTGGCCCTTTCTGGAG 882
QY 281 GluGlyProGluGluuAsnSerAlaTYrGluGlnLeuLeuSerArgLeuGluGluuLeuAla 300
Db 883 GAGGGCCCGGAAGAAACAGTCTCATGAGAGTGTGTCTCGCTGGAAATAATCGCT 942
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspLLeuSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGGCTCAGAACTCAGGTCCAGACCTGAGATATCTGCACTCTGCTCTGTAC 1002
QY 321 PheSerArgTYrPheGlnTYrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAGCCGCTACTTCCAATATAGAGGGGTCTGTGACTACACCGCCCTGTGCCAGGGGTTC 1062
QY 341 ILeTPTThrValPheAsnGlnThrValMetLeuSerAlaGlyGlnLeuHisStrLeuSer 360
Db 1063 ATCTGAGCTGTGTTTAAACAGACAGTGAAGTGAAGTGTCAACAGCTCCACACCTCTCT 1122
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgLLeuThrGlnPro 380
Db 1123 GACACCTGTGGGAGCTGTGTACTCTGGCTCAAGCTTAACCTCCAGACGACGAGCT 1182
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1183 TTGAATGGGCGAGTATGAGGCTCTCTCTGTGTGAGGTGAGACGAGTCTCTCGGGCT 1242
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLLeuAlaLeuValPhe 420
Db 1243 GCTGAGCAAGTCCACACTGAATTCGTGCTGTGTGTGTGACATCTTACCTCTGTGTTTT 1302
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCTCTTTTGT 1362
QY 441 ArgGlyThrLeuGlyGlyValSerTYrArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGGAACCAAGGGGGTGTGAGCTACCGCCAGAGAGGTAGCCGAGACTGGAAGCC 1419

RESULT 9
US-09-954-456-726
Sequence 726, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patencin version 3.0
SEQ ID NO 726
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-726
Alignment Scores:
Pred. No.: 9,97e-228 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-967-237A-2 (1-459) x US-09-954-456-726 (1-1552)
QY 1 MetAlaProLeuCysPProSerProTrpLeuProLeuLeuLeuProAlaProAlaProGly 20
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QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACCTGTGCAACTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 162
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGlyuAspAspProLeu 60
Db 163 CCCCAGATGACAGAGAGATTCCCCCTTGGAGAGGAGCTCTTCTGGGGAAGATGACCACTG 222
QY 61 GlyGluGluuAspLeuProSerGluGluuAspSerProArgGluGluuAspProGlyGlu 80
Db 223 GCGGAGAGAGATCTGCCCCAGTGAAGAGATTCACCAGAGAGAGATCCACCCGAGAG 282
QY 81 GluAspLeuProGlyGlyGlyuAspLeuProGlyGluGluuAspLeuProGluValLysPro 100
Db 283 GAGGATCTACTCTGAGAGAGAGATCTACTGAGAGAGAGATCTACTGAAATTAAAGCT 342
QY 101 LysSerGluGluGlySerLeuGluuAspLeuProThrValGluuLapProGly 120
Db 343 AAATAGAAAGAGAGGCTCTCTGAAATAGAGATCTACTGTTAGGCTCTCTGGA 402

Db 643 AGTGTCAACAGTACCCCTCTCTGGGGCTAGAGATGCTGTGGTCCCGGGGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleThrProGlyAlaAlaGlyArgProGlySerGlnHisIleThr 240
Db 703 CGGGCTGTGACAGCTGATCTGTGACGTGGGGGCTGTGAGGTGTCGGGGCTGGAGCACT 762
Qy 241 ValGlnGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCCCTTCCCTCCGAGATCCAGTGTGCTTCACTACAGACCCCTTGGC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTGACGAGAGCTTGGGGGCGCCGGAGGCGCTGGCGGTGTGGCGCCCTTCTGGAG 882
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 883 GAGGCGCCGGAGAAACAGATGCTATAGCAGTGTGCTGTCCGCTTGGAAATAATCCCT 942
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGGCTCAGAGACTCAGGTCCAGAGACTGGACATATCTGCACCTCTGCTCTGAC 1002
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAAGCCCTACTTCCATATGAGGGGTCTGTGACTACACCGCCCTGTGGCCAGGGGTGC 1062
Qy 341 IleThrPheValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisIleThrLeuSer 360
Db 1063 ATCTGAGACTGTGTTAACCAAGACAGTGAATGCTGAATGCTTAAGCACTCCACACCTCTCT 1122
Qy 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCCCTGTGGGAGCTGTGTGACTCTGGCTACAGCTGAACCTCCGAGCAGCAGGCT 1182
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProAla 400
Db 1183 TTGAATGGCGAGATTAAGAGGCTCTTCCCTGTGAGTGAAGCAGACAGTCCCTGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTAGCCAGTCCAGCTAATTCCTGCTGTGTGACATCTCAAGCCCTGATTTT 1302
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCTCTCTTTTCTGTCAACAGGCTCCGCTTCTGTGCAATGATGAAGGACAGACAGA 1362
Qy 441 ArgGlyThrIlyGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGGAACCAAGGGGGTGTGAGCTACCGCCAGAGAGTAAAGCGAGACTGGAGCC 1419

RESULT 11
US-09-873-367C-516
; Sequence 516, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Andrese, Gregory
; APPLICANT: Augustus, Weena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873, 367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236, 891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236, 842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244, 867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245, 084

; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 516
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-516

Alignment Scores:
Pred. No.: 9,976-228 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-967-237A-2 (1-459) x US-09-873-367C-516 (1-1552)

Qy 1 MetaLAPProLeuCyProSerProThrLeuProLeuLeuIleProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGGCCCGAGCCCTGTGCTCTCTGTGATCCGGCCCTGTCCAGGC 102
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACGTGCAACTGCTCTCTCTCACTGCTGCTTGTGAGCTCTTCATCCCAAGAGTTG 162
Qy 41 ProArgMetGlnLysAspSerProLeuGlyGlySerSerGlyLysAspAspProLeu 60
Db 163 CCCCGATGACAGAGGATTCCTCCCTTGGAGAGAGCTTCTTGGGGAGATGACCCACTG 222
Qy 61 GlyGluGluAspLeuProSerGluLysAspSerProArgGluGluAspProGlyLys 80
Db 223 GCGAGAGAGATCTGCCCAAGAGATTCACCGAGAGAGATCCACCGAGAG 282
Qy 81 GluAspLeuProGlyGlyGluLysAspProGlyGlyGluAspLeuProGluValLysPro 100
Db 283 GAGATCTACTGAGAGAGAGATCTACTGAGAGAGAGATCTACCGAAGTTAAGCT 342
Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 343 AAATCAGAAAGAGGGCTCCCTGAAGTAAAGATTAAGTACTGTTGAGGCTCTTGA 402
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 403 GATCTCAAGAACCCCAAGATTAATGCCACAGGACAAAGAGAGATCAAGATAT 462
Qy 141 TyrArgTyrGlyGlyAspProProThrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGGCTATGAGAGCGAACCGCCCTGGCCCGGGGTGTCCAGGCTGGCGGGCGCTTC 522
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuAspProLeu 180
Db 523 CAGTCCCGGGGTGATATCCGCCACAGCTCCGCCCTTGTGCCGGGCCCTGCCCTGTG 582
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis 200
Db 583 GAACCTCTGGGCTTCCAGCTCCCGCTCCCAAPACTGGCGCTGCGAACAATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 643 AGTGTCAACAGTACCCCTCTCTGGGCTAGAGATGCTGTGGTCCCGGGCGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleThrProGlyAlaAlaGlyArgProGlySerGlnHisIleThr 240
Db 703 CGGGCTGTGACAGCTGATCTGTGACGTGGGGGCTGTGAGGTGTCGGGGCTGGAGCACT 762
Qy 241 ValGlnGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCCCTTCCCTCCGAGATCCAGTGTGCTTCACTACAGACCCCTTGGC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280

Db 823 AGAGTTGACGAGCCCTTGGGGCCGCCGGAGGCGCTGGCCGTGTGGCCGCTTCTTGAG 882
Qy 281 GtuglyProglugluanseralatyrGtugluInleuanserAryleugluInleuA 300
Db 883 GAGGGCCCGAAGAAACAGTGTCTATGACAGTGTCTGTCTGCTTGAAAGAAATGCT 942
Qy 301 GtugluInlyserGtugluInvalProglyLeuaspileseralaleuProserAsp 320
Db 943 GAGGAAGCTCAGAGACTCAGGTCCAGGACTGGAACATATGTGACTCTGCTTGAC 1002
Qy 321 PheSerArgTyrPheGlnTyrGtuglySerleuThrProProcyValagInglyVal 340
Db 1003 TTCAGCGCTACTTCCAAATATGAGGGGTCTCTGACTACCGCCCTGTGGCAGGTC 1062
Qy 341 TleThrValPheansGlnThValMetLeuSerAlaysgInleuHsthrLeuSer 360
Db 1063 ATCTGAGCTGTGTATACACAGCTATGCTGAGTGTAGAGCTCCACACCTCTCT 1122
Qy 361 AspThrLeuTyrGlyProglyAspSerArgleuGlnleuansphearGalathrInPro 380
Db 1123 GACACCTGTGGGAGCTGGTGACTTCGGCTACAGCTGAACCTCCGAGCGACGACCT 1182
Qy 381 LeuanslyArgValIleGluAlaSerPheProAlaIyValAspSerSerProArgAla 400
Db 1183 TTGATGCGCGAGTATGAGGCTCTCTCTGCTGAGTGAAGCAGCAGTCTCGGGCT 1242
Qy 401 AlagluProValGlnleuanserCyaleuAlaIaglyAspIleleuAlaLeuValPhe 420
Db 1243 GCTGAGCAGATCCAGCTGAATTCCTGCTGGCTGCTGTGACATCCAGCCCTGTTT 1302
Qy 421 GlyleuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHsArg 440
Db 1303 GGCCTCTTTTGTCTGCTACACAGCGTGGCTTCTTGTGCAAGTGAAGAGCAGACAGA 1362
Qy 441 ArgGlyThrlysglyValiserTyrArgProAlaGluValIagluThrGlyAla 459
Db 1363 AGGGAAACAAAGGGGTGTGAGCTACCGCCACAGAGGTAGCGAGACTGAGCC 1419

RESULT 12
US-09-968-007A-213
; Sequence 213, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 213
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-213

Alignment Scores:
Pred. No.: 9,97e-228
Score: 2424.00
Percent Similarity: 100.00%

Length: 1552
Matches: 459
Conservative: 0

Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 11
Gaps: 0
US-09-967-237a-2 (1-459) x US-09-968-007A-213 (1-1552)
Qy 1 MetAlaProleuCyasProSerProTyrProleuLeuIleProAlaProAlaProgly 20
Db 43 ATGGCTCCCTGTGGCCCAAGCCCTGCTGCTCTGTGATCCCGGCCCTGCTCAGGC 102
Qy 21 LeuThrValGlnleuLeuSerleuLeuLeuMetProValHsProGlnArgleu 40
Db 103 CTGACTGTGAACTGTCTGTGCTGCTGCTGTCTGTATGCTGTCAATCCCGAGAGTTG 162
Qy 41 ProArgMetGlnIleuAspSerProleuGlyGlyIySerSerGlyIleuAspAppProleu 60
Db 163 CCCCGATGAGAGAGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAAGATGACCCACTG 222
Qy 61 GlyGluIleuAspLeuProSerGluIleuAspSerProArgGluIleuAspProProgly 80
Db 223 GCGAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCCGAGAG 282
Qy 81 GluAspLeuProGlyGluIleuAspLeuProGlyGluIleuAspLeuProGlyIleuPro 100
Db 283 GAGGATCTTACTGTGAGAGAGATCTTACTGTGAGAGAGATCTTACTGTGAGATTAAGCT 342
Qy 101 IySerGlyGluIleuGlySerleuLyLeuGluAspLeuProThrValGluAlaProgly 120
Db 343 AAATCAGAAAGAGGCTCCCTGAAATTAGAGATCTTACTGTGAGATTAAGCT 402
Qy 121 AspProGlnIleuProGlnleuanseralHsArgAspLyGlyIleuAspArgInsThrHs 140
Db 403 GATCTCAAGAAACCCAGATATATGCCACAGGGAAGAAAGAGGATGCCAGAGTCAAT 462
Qy 141 TrrArgTyrGlyIyAspProProTyrProArgValSerProAlaCyAlaGlyArgPhe 160
Db 463 TGGCGCTATGAGAGCCAGCCCGCTGGCCCGGGGTGTCCACAGCTGGCGGGCCGGTTC 522
Qy 161 GlnSerProValAspIleArgProGlnleuAlaAlaPheCyasProAlaLeuArgProleu 180
Db 523 CATTCCTCCGCTGATATCCGCCCCAGCTGCCGCTTGTGCCCGCCCTGCGCCCTG 582
Qy 181 GlnleuLeuGlyPheGlnleuProProleuProGlnleuArgleuArgansenglyHs 200
Db 583 GAACCTCTGGGCTTCAGACTCCCGCCCTCCAGAACTGGCTGGCAACAATGGCCAC 642
Qy 201 SerValGlnleuThrleuProProGlyIleuGlnMetAlaLeuGlyProGlyArgGly 220
Db 643 AGTGTCACTGACCTCTGCTGGGCTTGAAGATGCTGTGGTCCCGGCGGAGTAC 702
Qy 221 ArgAlaLeuGlnleuHsleuHsIstrGlyAlaIaglyArgProglySerGlnHsthr 240
Db 703 CGGGCTCTGAGTGTATGCACTGGGGGGCTGCGAGTGTCTCGGGCTCGAGCACT 762
Qy 241 ValGluGlyHsArgPheProAlaGluIleHsValValHsleuSerThrAlaPheAla 260
Db 763 GTGAAGGCCACCGTTTCTCTGCGAGATCCAGTGTTCACCTCGACACCGCTTGGC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyIleuAlaValleuAlaAlaPheleuGlu 280
Db 823 AGAGTTGACGAGGCTTGGGGCCCGGGAGGCTGTGGCTGTGGCCGCTTCTTGAG 882
Qy 281 GtuglyProglugluanseralatyrGtugluInleuanserAryleugluInleuA 300
Db 883 GAGGGCCCGAAGAAACAGTGTCTATGACAGTGTCTGTCTGCTTGAAAGAAATGCT 942
Qy 301 GtugluInlyserGtugluInvalProglyLeuaspileseralaleuProserAsp 320
Db 943 GAGGAAGCTCAGAGACTCAGGTCCAGGACTGGAACATATGTGACTCTGCTTGAC 1002
Qy 321 PheSerArgTyrPheGlnTyrGtuglySerleuThrProProcyValagInglyVal 340
Db 1003 TTCAGCGCTACTTCCAAATATGAGGGGTCTCTGACTACCGCCCTGTGGCAGGTC 1062


```

, GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIORITY APPLICATION NUMBER: 60/380,770
PRIORITY FILING DATE: 2002-05-14
, NUMBER OF SEQ ID NOS: 2699
, SEQ ID NO 574
, LENGTH: 1552
, TYPE: DNA
, ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
, DATABASE ACCESSION NUMBER: NM_001216
, DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574

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Alignment Scores:

Pred. No.:	9.97e-228	Length:	1552
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-967-237A-2 (1-459) x US-10-172-118-574 (1-1552)

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Qy	21	LeuThrValGluLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnATyGlu	40
Db	103	CTCAGTGTCAACTGTGTCTGTCACTGTCTCTTCTATGTCTTCCATCCCCAGAGTTG	1630
Qy	41	ProArgMetGluGluAspSerProLeuGlyGlyIYserSerGlyGluAspAspProLeu	60
Db	163	CCCCGGATGCAAGAGGATTCCTCCCTTGGAGAGAGGCTCTTCTGGGAGAATGATCCACTG	2220
Qy	61	GlyGlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80
Db	223	GCGGAGAGAGATCTGCCAGTAAAGAGATTCCACCAAGAGAGAGATCCACCGGAGAG	2820
Qy	81	GluAspLeuProGlyGlyGluGluAspLeuProGlyGlyGluGluAspLeuProGluValIYsPro	100
Db	283	GAGGATCTTAACTGTGAAGAGGATCTTAAGTGAAGAGAGATTTACTGTAAGTTAAGCT	3420
Qy	101	IYsSerGlyGluGlyGlySerLeuIYsLeuGluAspLeuProThrValGlu1aPProGly	120
Db	343	AAATAGAGAGAGAGGCTCCCTGAAGTTAAGAGATCTACCTGTGAGGCTCTCGGA	4020
Qy	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspIYsGlyGluIYsAspGlnSerHis	140
Db	403	GATCTCTAAGAAACCCCAAGATAATATGCCACAGGGAACAAAGAGGGATGACCAAGATCAT	4620
Qy	141	TrpArgTyGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe	160
Db	463	TGGCCCTATGAGAGGACCCGCTTGCGCCCGGGGTCTCCCACTCGCGGCGCCCTTC	5220
Qy	161	GlnSerProValAspIleArgProGlnLeuAla1aPheCysProAlaLeuAspProLeu	180
Db	523	CAGTCCCGGTGAATATCGCCCCCAAGCTGCGGCTTGTGCCCCGGCCCTGCCCCCTG	5820
Qy	181	GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlnHis	200

Db	583	GAACCTCTGGGGCTTCACAGTCCCGCGCGCTCCAGAACTCCGCTGGCGAACATGGCCAC	642
Qy	201	SeRVaLgInLeuThrLeuProProglYleuGInMeTAlaLeuGlyProglYArgrglYr	220
Db	643	AGTGTGCAACTGACCCCTGCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGAGGTAC	702
Qy	221	ArGAlaLeuGInLeuHISleuHISrTrpGlYAlaIaGlyArgrProglYSeGrLWHISrTr	240
Db	703	CGGGCTCTGCAGCTGCATCTGCACTCGGGGGGCTGAGAGGTCTCCGGCTCCGAGCACACT	762
Qy	241	ValGInGlyHISArgrPheProAlaGInuLeHISValaValHISLeuSerThrAlaPheAla	260
Db	763	GTGAAAGGCGACCGTTCCTTCCTCCGAGATTCACAGrGrTTCACTTACAGCACCGCTTGGC	822
Qy	261	ArGVaLaSpGInuAlaLeuGlyArGrProglYglYleuAlaValaLeuAlaAlaPheLeuGIn	280
Db	823	AGAGTTGACGAGGCTTGGGGGGCGCCGGGAGGCGTGGCCGTGTGGCCGCTTTCGTGGAG	882
Qy	281	GIuGIuGIProGIuGIuASerSerAlArYrGIuGInLeuLeuSerArgrLeuGIuGIuLeaIa	300
Db	883	GAGGGCCCCGGAAGAAACAGTGCCTATAGCGATTCGTCTCGCTTGGGAACAAATTCGCT	942
Qy	301	GIuGIuGIYSerGIuThrGIuValaProGIuLeuASpIISerAlaLeuLeuProSerASp	320
Db	943	GAGGAGGCTCAGAGACTCAGGTCCCAAGACTGAGCAATrTGCACCTCCGCTCTGCAC	1000
Qy	321	PheSerArgrYrPheGInTrYrGIuGIYSerLeuThrTrhProProCYaAlaGInGIYAl	340
Db	1003	TTCAACCGCTACTTCATATAGAGGGATCTGTGACTACACGCGCTGTGCCAGGAGTGC	1060
Qy	341	ILeTrPThrValPheASrGInThrYAlMeLeuSerAlaYvGIuLeuHISrThrLeuSer	360
Db	1063	ATCTGGACTGTGTTCATACCACTGATGTCTGATGTCTTAAGACACTCCACACCTCTCT	1122
Qy	361	ASpThrLeuTrpGIYProGIYASpSerArgrLeuGInLeuASrPheArgrAlaThrGInPro	380
Db	1123	GACACCTCTGTGGGACCTGTGCACCTCTCGGCTCAACGCTGMACTTCCGACGACGACGCT	1180
Qy	381	LeuHENGlyArGVaLIleGInuAlaSerPheProAlaGIYAlaASpSerSerProArgrAla	400
Db	1183	TTGAATGGGCGAGGTATTGAGGCGCTCTTCCTCGCTGAGAGTGGACAGCAGTCTCGGGCT	1240
Qy	401	AlaGInUProValGInLeuASrSerCYsleuAlaAlaGIYASpIISleuAlaLeuValPhe	420
Db	1243	GCTGAGCGAGTCCAGACTGAATTCCTGCTGTGTGTGTGATCTTAAGCCCTGTGTTTT	1300
Qy	421	GIYleuLeuPheAlaValTrhSerValaAlaPheLeuValGInMeArGrGIuHISArgr	440
Db	1303	GGCTCTCTTTTGTGTGTGTACCAAGGCTCCGCTTCTGTGTGCATAGAAAGGACGACGACA	1360
Qy	441	ArGrGIYThrYvGIYGIYValaSerYrArgrProAlaGInuAlaAlaGInuThrGIYAla	459
Db	1363	AGGGGAACCAAGGGGGGTGTAGACTACCGCCGAGAGAGTATGCGAAGCTGAGACC	1419

Search completed: August 20, 2005, 01:45:36
Job time : 911 secs

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